

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:28:11 ; Search time 20004.5 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259C-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;


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Best Local Similarity 100.0%; Pred. No. 2,3e-159;
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VERSION AY032736.1 GI:14029162
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AUTHORS Liu, L. and Yuan, L.
TITLE Human alpha-2A adrenergic receptor gene and the genotype of -1296
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3612)
AUTHORS Liu, L. and Yuan, L.
TITLE Direct Submission
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General Hospital of Airforce, Fucheng Road No. 30, Beijing 100036,
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Db	1540	CAGATGCCNAGGCTGCGACCCGCGGTGCCACCCAGCGCGCGGGGTCCGAGACCGCGTCCGC	1599		

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Qy	781	CC	GGGGGGCGCAGAGGCCGAACCGCTGCCACCCAGCTCAACGGCGCCCTTGGCGAGCC	840
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Qy	841	GC	CGCGCGCGGGCGCGGACACCGAGCGCGCTGACCTGGAGGAGAGCTCGTCTTCGAC	900
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Qy	901	CAC	CCGAGCGGGCTCCAGGGCCCCGAGACCCGAGCGCGGTCCC CGGGCAAGCGCAAG	960
Db	1780	CAC	CCGAGCGGGCTCCAGGGCCCCGAGACCCGAGCGCGGTCCC CGGGCAAGCGCAAG	1839
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Qy	1021	GG	ATCGGGACCGCGGTGACGGCCCGGGGAGAGCGCGTGGGGCTGCACAGGCGTCG	1080
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LOCUS	AL158163				
DEFINITION	Human DNA sequence from clone RP11-348N5 on chromosome 10, complete sequence.				
ACCESSION	AL158163				
VERSION	AL158163.11	GI:17384427			
KEYWORDS	HTG.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 204908)				
TITLE	Johnson, C.				
JOURNAL	Direct Submission				
COMMENT	Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 5, 2001 this sequence version replaced gi:16944857. On Dec 5, 2001 this sequence version replaced gi:16944857. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=				

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at

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 of Pieter de Jong, For further details see
<http://www.chori.org/bacpac/home.htm>

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FEATURES

source

1. 204908

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="10"

/clone="RP11-348N5"

/clone.lib="RP11-11.2"

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RESULT 7

AX350513

Sequence 25 from Patent WO0179561.

AX350513

AX350513.1 GI:18616108

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source

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Gaps				0
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QY 601 TGCATCGGTCTCTTCTGCTCTGCTCTGCTCATCATGATCTCTGCTGCTGCTGCTTAC 660
DB 2678 TGCATCGGTCTCTTCTGCTCTGCTCTGCTCATCATGATCTCTGCTGCTGCTGCTTAC 2737
QY 661 CAGATGCCAAGGCTCGACCGCGGTGACCAACCGCGCGGCTCGGACCGCGCTCGCC 720
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DB 2918 GCGCCGCGCGGGGCGCGCGACCCAGCCGCTGGAACCTGAGAGAGAGCTGCTTTCGAC 2977
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QY 1140 CGGAGTGTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
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DB 3337 GTTGAACCGCGTCTATCATCATCTTCAACCAAGATTTCCGCGCGCTTCAAGAAAGAT 3396
QY 1320 CTTCTGTCGGGGGCGAGGAGCGGATCGTG 1350
DB 3397 CTTCTGTCGGGGGCGAGGAGCGGATCGTG 3427
RESULT 10
HUMADRA Human platelet alpha-2-adrenergic receptor gene, complete cds.
LOCUS M18415.1 GI:178191
DEFINITION alpha-2-adrenergic receptor; alpha-adrenergic receptor.
ACCESSION M18415.1
VERSION Human (lambda-EMBL 3 library) DNA.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
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Best Local Similarity	99.5%; Pred. No 1.ee-155;				
Matches 1344; Conservative	0; Mismatches 5; Indels 2; Gaps 2;				
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Qy 61	GGCGGCGCCCGGACACCCCTTACTCCCTGACGTGACGCTGACGCTGTGTGCTGTGCTGGCC	120			
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Qy 241	CTGTGGCCACGCTCGTCATCCCTTTCTCGGTGGCCCAACGAGGTCACTGGGTACTGGTAC	300			
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Qy 301	TTGCGCAAGGCTTGGTGGAGATCTACTGTGGCGCTCGACGTGCTCTTCTGCACGTGCTCC	360			
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Qy 481	TCGGCCGTCTATCTCTTTCCGCGCCTCATCTCCATCGAAGAAAGGCGCGCGCGCGGC	540			
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Qy 541	CCGACGCGGCGGACGCGCGTGGAGATCAACGACAGAGTGGTACGTATCTCGTCG	600			
Db 599	CCGACGCGGCGGACGCGCGTGGAGATCAACGACAGAGTGGTACGTATCTCGTCG	658			
Qy 601	TGCATCGGCTCTTTCTTTCGCTCCCTGCTCATCATGATCTCTGCTACGTGGCATCTAC	660			
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Qy 661	CAGATCGCCAAAGCTCGCACCCCGCTGCCACCCAGCGCGCGGGTCCGACGCGCTCGCC	720			
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Qy	781	CCGGGGGCGCAGAGGCCGAACCGCTGCCCAACAGCTCAA	CGCGCCCTCGCGAGCC	840
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Qy	961	CGCCAGCGAGCCAGGTGAAGCCGGCGAGCAGCTTCGCGCGCGCGGGCGGGGGCGAGC	102	
Db	1019	CGCCAGCGAGCCAGGTGAAGCCGGCGAGCAGCTTCGCGCGCGCGGGCGGGGGCGAGC	107	
Qy	1021	GGGATCGGGAGCGCGCTGCAGAGGCCGGGGGAGGAGCGGTGGGGCTGCCAAGGCGTCG	108	
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Db	1138	CGCTGGCGCGGGCGGCGAGAACTCAGAAAGCGCTTCACGTTCTGCTGGCCGTCGTCTCAT	119	
Qy	1140	CGGAGTGTTCGTGGTGTGTGTTCCCTTCCTTCACCTACAGCTACAGCTCACGGCCGTCGG	119	
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Qy	1200	GTGCTCCGTCCGACGACGCTCTTCAAAATCTCTCTGTTCTGGTCTGGCTACTGCAACAGCTC	125	
Db	1258	GTGCTCCGTCCGACGACGCTCTTCAAAATCTCTCTGTTCTGGTCTACTGCAACAGCTC	131	
Qy	1260	GTTGAACCCGGTCATCTACACCATCTTCAACCAAGATTTCCGCGCGGCTTCAAGAAAT	131	
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Qy	1320	CCCTGTGGGGGACAGGACGGATCGTG	1350	
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RESULT 11
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LOCUS      1728 bp      DNA      linear      MAM 27-APR-1993
DEFINITION Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
ACCESSION J05652
VERSION    J05652.1 GI:164303
KEYWORDS   alpha-2A-adrenergic receptor.
SOURCE     Porcine liver DNA.
ORGANISM   Sus scrofa
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            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 1728)
            Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J. Jr.
            and Limbird, L.E.
            Unpublished (1990)
REFERENCE  2 (bases 70 to 1582)
            Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cragoe, E.J. Jr.
            and Limbird, L.E.
            Cloning, sequencing, and expression of the gene encoding the
            porcine alpha 2-adrenergic receptor. Allosteric modulation by Na+,
            H+, and amiloride analogs
            J. Biol. Chem. 265 (28), 17307-17317 (1990)
MEDLINE    91009167
PUBMED     2170371
COMMENT    Draft entry and computer-readable sequence for [J. Biol. Chem.
            (1990) In press] kindly submitted
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BASE COUNT 268 a 590 c 562 g 308 t

Query Match 85.2%; Score 1150; DB 4; Length 1728;
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ACCESSION U25722
VERSION 1
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SOURCE Cavia porcellus.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 2291) Porter, A.C., Richman, J.G. and
AUTHORS Svensson, S.P., Bailey, T.J., Regan, J.W.
TITLE Heterologous expression of the cloned guinea pig alpha 2A, alpha
2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene
Biochem. Pharmacol. 51 (3), 291-300 (1996)
JOURNAL MEDLINE 96152573
PUBMED 8573196
REFERENCE 2 (bases 1 to 2291)
AUTHORS Richman, J.G.
TITLE Direct Submission
JOURNAL Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA
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Qy	661	CAGATCGGCAAG	CGTCCGACCCCGGTGCACACCGACCGCGGGTTCGGACGC---CGTC	717					
Db	706	CAAAATAGCC	AGCGCCGCAACCCCGGTGCACACCGACCGCGGAGTCCGGACGCCACGCC	765					
Qy	718	GCSCGCGCGCG	GGGGGACCGAGCGCAGGCCCAACCGTCTGGGCCCCCGAGCGGCG	777					
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Db	781	ACCGGGGCGCGAGCGCGAGCGCTGCCCAACCGAGCTTAACGGCGCCCGCGGGGAGCGCC	840	
QY	841	GGCGCGCGCGCGCGCGACACCGAGCGCTGGACCTGGAGGAGAGCTCGTCTTCGCGAC	900	
Db	841	GGCGCCACCGCGCGCGCGACCGGGATGCGCTTGGACCTTAGAGGAGAGTTCGTCTCGCAG	900	
QY	901	CACGCGAGCGGCGCTCCAGGGCGCGCAGACCCCGAGCGCGGTCCCGGGGCAAAAGGCAAG	960	
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VERSION	M62372.1 GI:206615			
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ORGANISM	Rattus norvegicus			
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AUTHORS	Lanier,S.M., Downing,S., Duzic,E. and Homey,C.J.			
TITLE	Isolation of rat genomic clones encoding subtypes of the alpha			
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JOURNAL	J. Biol. Chem. 266 (16), 10470-10478 (1991)			
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DEFINITION	Bos taurus alpha2D adrenergic receptor gene, complete cds.	ACCESSION	U79030	VERSION	U79030.1	GI:3282232	
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REFERENCE	1 (bases 1 to 2923)	AUTHORS	Venkataraman, V., Duda, T. and Sharma, R.K.	TITLE	The bovine alpha 2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor		
JOURNAL	Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)	MEDLINE	9811113	PUBMED	9450652		
REFERENCE	2 (bases 1 to 2923)	AUTHORS	Venkataraman, V., Duda, T.M. and Sharma, R.K.	TITLE	Direct Submission		
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1 (bases 1 to 204317)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-358H2
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS

2 (bases 1 to 204317)
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Direct Submission
Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE
AUTHORS

3 (bases 1 to 204317)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 6, 2002 this sequence version replaced gi:21313866.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L23807

Center clone name: 358_H.2

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731
Consensus quality: 19709 bases at least Q40
Consensus quality: 200412 bases at least Q30
Consensus quality: 201149 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 202017; sum-of-contigs
Quality coverage: 6.3 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 7387: contig of 7387 bp in length

* 7388 7487: gap of 100 bp

* 7488 7956: contig of 469 bp in length

* 7957 8056: gap of 100 bp

* 8057 9200: contig of 1144 bp in length

* 9201 9300: gap of 100 bp

* 9301 10747: contig of 1447 bp in length

* 10748 10847: gap of 100 bp

* 10848 12877: contig of 2030 bp in length

* 12878 12977: gap of 100 bp

* 12978 15172: contig of 2195 bp in length

* 15173 15272: gap of 100 bp

* 15273 18061: contig of 2789 bp in length

* 18062 18161: gap of 100 bp

* 18162 21071: contig of 2910 bp in length

* 21072 21171: gap of 100 bp

* 21172 24003: contig of 2832 bp in length

* 24004 24103: gap of 100 bp

* 24104 27175: contig of 3072 bp in length

* 27176 27275: gap of 100 bp

* 27276 30561: contig of 3286 bp in length

* 30562 30661: gap of 100 bp

* 30662 66787: contig of 36106 bp in length

* 66788 66887: gap of 100 bp

* 66888 73300: contig of 6433 bp in length

* 73301 73400: gap of 100 bp

* 73401 78880: contig of 5480 bp in length

* 78881 78980: gap of 100 bp

* 78981 89075: contig of 10095 bp in length

* 89076 89175: gap of 100 bp

* 89176 98581: contig of 9406 bp in length

* 98582 98681: gap of 100 bp

* 98682 105311: contig of 6630 bp in length

* 105312 105411: gap of 100 bp

* 105412 122788: contig of 17377 bp in length

* 122789 122888: gap of 100 bp

* 122889 132289: contig of 9401 bp in length

* 132290 132389: gap of 100 bp

* 132390 144818: contig of 12429 bp in length

* 144819 144918: gap of 100 bp

* 144919 159101: contig of 14183 bp in length

* 159102 159201: gap of 100 bp

* 159202 177288: contig of 18087 bp in length

* 177289 177388: gap of 100 bp

* 177389 201231: contig of 23843 bp in length

* 201232 201331: gap of 100 bp

* 201332 204317: contig of 2986 bp in length.

Location/Qualifiers

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/organism="Mus musculus"

/db xref="taxon:10090"

/clone="RP23-358H2"

/clone_lib="RPCI-23 Female Mouse BAC"

1. .7387

/note="assembly_fragment"

misc_feature

RGFGAAGPGASGSGHGERGGGAKASRWGRONREKRTFTVLAVVIGVFWVWCPFFP
 TYTLIAVGCPVPSQLPFFFWFGYCNSSLNPVIYTFNHDFFRAFKKILCRGDRKRIV

BASE COUNT 229 a 481 c 467 g 277 t
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Query Match 84.4%; Score 34.6; DB 10; Length 1454;
 Best Local Similarity 90.2%; Pred. No. 0.94; 4; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 780 GGGGCGCCGATCGACGAGCCCAACGGCTGGGCCCGGAGCG 820

RESULT 12
 RRU79031 1552 bp mRNA linear ROD 14-JUN-2000
 LOCUS Rattus norvegicus alpha2D adrenergic receptor mRNA, complete cds.
 DEFINITION
 U79031
 VERSION
 U79031.1 GI:3282234
 KEYWORDS
 Rattus norvegicus.
 SOURCE
 Rattus norvegicus.
 ORGANISM

REFERENCE
 1 (bases 1 to 1552)
 Chaberg, S.C., Duda, T., Rhine, J.A. and Sharma, R.K.
 Molecular cloning, sequencing, and expression of an alpha
 2-adrenergic receptor complementary DNA from rat brain
 Mol. Cell. Biochem. 97 (2), 161-172 (1990)
 JOURNAL
 MEDLINE
 PUBMED
 91125329
 2177834

REFERENCE
 2 (bases 1 to 1552)
 Wypijewski, K., Duda, T. and Sharma, R.K.
 Structural, genetic and pharmacological identity of the rat alpha
 2-adrenergic receptor subtype ca2-47 and its molecular
 characterization in rat adrenal, adrenocortical carcinoma and
 bovine retina
 Mol. Cell. Biochem. 144 (2), 181-190 (1995)
 JOURNAL
 MEDLINE
 PUBMED
 95349580
 7623790

REFERENCE
 3 (bases 1 to 1552)
 Venkataraman, V., Duda, T.M. and Sharma, R.K.
 Direct Submission
 Submitted (20-NOV-1996) Cell Biology, UMDNJ-SOM, 2 Medical Ctr.
 Dr., Stratford, NJ 08084, USA
 JOURNAL
 LOCATION/Qualifiers

FEATURES
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BASE COUNT 244 a 504 c 498 g 306 t
 ORIGIN

Query Match 84.4%; Score 34.6; DB 10; Length 1552;
 Best Local Similarity 90.2%; Pred. No. 0.93;
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 780 GGGGCGCCGATCGACGAGCCCAACGGCTGGGCCCGGAGCG 820

RESULT 13
 PIGA2AR 1728 bp DNA linear MAM 27-APR-1993
 LOCUS Porcine alpha2A-adrenergic receptor (PORA2AR) gene, complete cds.
 DEFINITION
 J05652
 VERSION
 J05652.1 GI:164303
 KEYWORDS
 alpha-2A-adrenergic receptor.
 SOURCE
 Porcine liver DNA.
 ORGANISM

REFERENCE
 1 (bases 1 to 1728)
 Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J. Jr.
 and Limbird, L.E.
 Unpublished (1990)
 2 (bases 70 to 1582)
 Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kragoe, E.J. Jr.
 and Limbird, L.E.
 Cloning, sequencing, and expression of the gene encoding the
 porcine alpha 2-adrenergic receptor. Allosteric modulation by Na⁺,
 H⁺, and amiloride analogs
 J. Biol. Chem. 265 (28), 17307-17317 (1990)
 JOURNAL
 MEDLINE
 PUBMED
 91009167
 2170371

COMMENT
 Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) in press] kindly submitted
 by C.A. Guyer, 02-AUG-1990.
 FEATURES
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BASE COUNT 268 a 590 c 562 g 308 t
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Query Match 84.4%; Score 34.6; DB 4; Length 1728;
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 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 859 GGGGCGCCGATCGACGAGCCCAATGGCCTAGGCCCGGAGCG 899

RESULT 14
 AC113491/c 204317 bp DNA linear HTG 06-JUN-2002
 LOCUS Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
 DEFINITION
 AC113491
 VERSION
 AC113491.3 GI:21327601
 KEYWORDS
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 204317)
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 JOURNAL
 MEDLINE
 PUBMED
 2170371

COMMENT
 Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) in press] kindly submitted
 by C.A. Guyer, 02-AUG-1990.
 FEATURES
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BASE COUNT 268 a 590 c 562 g 308 t
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Query Match 84.4%; Score 34.6; DB 4; Length 1728;
 Best Local Similarity 90.2%; Pred. No. 0.91;
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 859 GGGGCGCCGATCGACGAGCCCAATGGCCTAGGCCCGGAGCG 899

RESULT 14
 AC113491/c 204317 bp DNA linear HTG 06-JUN-2002
 LOCUS Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
 DEFINITION
 AC113491
 VERSION
 AC113491.3 GI:21327601
 KEYWORDS
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 204317)
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 JOURNAL
 MEDLINE
 PUBMED
 2170371

COMMENT
 Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) in press] kindly submitted
 by C.A. Guyer, 02-AUG-1990.
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 PGEAPTRPDGDLDLDESSSEHAERPPQGPGRKAKTKASQVKGPSLPR
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BASE COUNT 268 a 590 c 562 g 308 t
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Query Match 84.4%; Score 34.6; DB 4; Length 1728;
 Best Local Similarity 90.2%; Pred. No. 0.91;
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Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 859 GGGGCGCCGATCGACGAGCCCAATGGCCTAGGCCCGGAGCG 899

RESULT 14
 AC113491/c 204317 bp DNA linear HTG 06-JUN-2002
 LOCUS Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
 DEFINITION
 AC113491
 VERSION
 AC113491.3 GI:21327601
 KEYWORDS
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 204317)
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 JOURNAL
 MEDLINE
 PUBMED
 2170371

COMMENT
 Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) in press] kindly submitted
 by C.A. Guyer, 02-AUG-1990.
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 SAVISFPLISIEKKGAGGQGPAPPSCKINDQKQYVSSIGSFAPCLIMILVYVR
 IQYIAKRTRVPPSRPDACAPPGADRPNGLPGERAGTAGAEPLPTOLNGA
 PGEAPTRPDGDLDLDESSSEHAERPPQGPGRKAKTKASQVKGPSLPR
 RGPAGAGGAGGGERAGAKASRWGRONREKRTFTVLAVVIGVFWVWCPFFP
 TYTLIAVGCSVPPTLTKFFFWFGYCNSSLNPVIYTFNHDFFRAFKKILCRGDRKRIV

BASE COUNT 268 a 590 c 562 g 308 t
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Query Match 84.4%; Score 34.6; DB 4; Length 1728;
 Best Local Similarity 90.2%; Pred. No. 0.91;
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGACCCAGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 859 GGGGCGCCGATCGACGAGCCCAATGGCCTAGGCCCGGAGCG 899

RESULT 14
 AC113491/c 204317 bp DNA linear HTG 06-JUN-2002
 LOCUS Mus musculus clone RP23-358H2, WORKING DRAFT SEQUENCE, 24 ordered
 DEFINITION
 AC113491
 VERSION
 AC113491.3 GI:21327601
 KEYWORDS
 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus

REFERENCE
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 HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 JOURNAL
 MEDLINE
 PUBMED
 2170371

COMMENT
 Draft entry and computer-readable sequence for [J. Biol. Chem.
 (1990) in press] kindly submitted
 by C.A. Guyer, 02-AUG-1990.
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 130..1482
 /note="alpha2A-adrenergic receptor (PORA2AR)"
 /codon_start=1
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 /translation="MGSLOPEAGNSWNGTEAPGGGARATPYSLQVTLTVCLAGLLM
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 SAVISFPLISIEKKGAGGQGPAPPSCKINDQKQYVSSIGSFAPCLIMILVYVR
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 PGEAPTRPDGDLDLDESSSEHAERPPQGPGRKAKTKASQVKGPSLPR
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Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 196299 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 196339

RESULT 9
AX350513 AX350513 1350 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 25 from Patent WO0179561.
DEFINITION
ACCESSION AX350513
VERSION AX350513.1 GI:18616108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Liggett,S.B. and Small,K.M.
AUTHORS Alpha-2 adrenergic receptor polymorphisms
TITLE Patent: WO 0179561-A 25 25-OCT-2001;
JOURNAL Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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/db_xref="taxon:9606" 220 t

BASE COUNT 199 a 489 c 442 g 220 t
ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.035;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
Db 730 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 770

RESULT 10
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LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
DEFINITION
ACCESSION AF316894
VERSION AF316894.1 GI:12698667
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191
REFERENCE
2 (bases 1 to 1353)
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
FEATURES
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gene
mRNA
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SAVISFPPLISIEKKGGGQPAEPKCEINDOKWIVISSCIGSFAPCLIMLVYVR
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variation
200 a 489 c 443 g 221 t
BASE COUNT
ORIGIN

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/notes="compared to wild type sequence presented in GenBank
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/frequency="Caucasians 0.004; African-Americans 0.05"
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QY 1 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 41
|||||
Db 730 GGGGGCACCAGCGCGAGCCCAACGGTCTGGGCCCGGAGCG 770

RESULT 11
MUSALP2ADB MUSALP2ADB 1454 bp DNA linear ROD 27-APR-1993
LOCUS Mouse alpha-2 adrenergic receptor, complete cds.
DEFINITION
ACCESSION M99377
VERSION M99377.1 GI:191882
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Mus musculus (strain 129/Sv) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1454)
AUTHORS Link,R., Daunt,D., Barsh,G., Chruscinski,A. and Kobilka,B.
TITLE Cloning of two mouse genes encoding alpha 2-adrenergic receptor
subtypes and identification of a single amino acid in the mouse
alpha 2-C10 homolog responsible for an interspecies variation in
antagonist binding
JOURNAL Mol. Pharmacol. 42 (1), 16-27 (1992)
MEDLINE 92342131
PUBMED 1353249
FEATURES
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CDS
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    Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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RESULT 2
HUMADRA
LOCUS
  AF281308 1353 bp DNA linear PRI 05-DEC-2000
DEFINITION
  Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
  cds.
ACCESSION
  AF281308
VERSION
  AF281308.1 GI:9652209
KEYWORDS
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SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1353)
  Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
  An asn to lys polymorphism in the third intracellular loop of the
  human alpha 2A-adrenergic receptor imparts enhanced
  agonist-promoted Gi coupling
  J. Biol. Chem. 275 (49), 38518-38523 (2000)
  20556293
  PUBMED
  10948191
REFERENCE
  2 (bases 1 to 1353)
  Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
  Direct Submission
  TITLE
  Submitted (22-JUN-2000) Internal Medicine, University of
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    |||||

RESULT 3
HUMADRA
LOCUS
  AF262016 1941 bp DNA linear PRI 22-AUG-2000
DEFINITION
  Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
ACCESSION
  AF262016
VERSION
  AF262016.2 GI:9864781
KEYWORDS
  .
SOURCE
  Homo sapiens.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1941)
  Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
  Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
  Cloning, sequencing, and expression of the gene coding for the
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  Science 238 (4827), 650-656 (1987)
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    |||||
  Db 788 GGGGGCCAGCGAGCGAGCCCAACGGTCTGGGCCCCGAGCG 828
    |||||

RESULT 4
AF262016
LOCUS
  AF262016 1941 bp DNA linear PRI 22-AUG-2000
DEFINITION
  Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
ACCESSION
  AF262016
VERSION
  AF262016.2 GI:9864781
KEYWORDS
  .
SOURCE
  Homo sapiens.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1941)

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:28:11 ; Search time 607.543 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259c-1_COPY_730_770

Perfect score: 41
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*

3: gb_in:*

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9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: gb_wa:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	100.0	1353	9	AF281308	AF281308 Homo sapi
3	41	100.0	1521	9	HUMADRA	M18415 Human plate
4	41	100.0	1941	9	AF262016	AF262016 Homo sapi
5	41	100.0	3604	9	HUMADRA2R	M23533 Human alpha
6	41	100.0	3612	9	AY032736	AY032736 Homo sapi
7	41	100.0	3653	9	AF284095	AF284095 Homo sapi
8	41	100.0	204908	9	AL158163	AL158163 Human DNA
9	39.4	96.1	1350	6	AX350513	AX350513 Sequence
10	39.4	96.1	1353	9	AF316894	AF316894 Homo sapi
11	34.6	84.4	1454	10	MUSALP2ADB	M99377 Mouse alpha
12	34.6	84.4	1552	10	RRU79031	U79031 Rattus norv
13	34.6	84.4	1728	4	PIGA2AR	J05652 Porcine alp
14	34.6	84.4	204317	2	AC113491	AC113491 Mus muscu
15	33	80.5	2923	4	BTU79030	U79030 Bos taurus
16	31.4	76.6	1380	10	RATRG20	M62372 Rat alpha-2
17	31.4	76.6	2291	10	CPU25722	U25722 Cavia porce
18	25	61.0	7353	6	AX344974	AX344974 Sequence
19	25	61.0	7353	6	AX348495	AX348495 Sequence
20	25	61.0	51146	2	AC090342	AC090342 Homo sapi
21	25	61.0	64711	2	AC114552	AC114552 Mus muscu
22	24.2	59.0	163156	2	AF004085	AF004085 Oryza sat
23	23.8	58.0	127128	2	AC105677	AC105677 Rattus no
24	23.6	57.6	11378	1	AE002058	AE002058 Deinococc
25	23.6	57.6	43147	1	SC4A10	AL109663 Streptomy
26	23.6	57.6	126141	2	AL356300	AL356300 Homo sapi
27	23.6	57.6	163801	2	AC025224	AC025224 Homo sapi
28	23.6	57.6	195076	9	AL391357	AL391357 Human DNA
29	23.4	57.1	1263	9	HSACAA1	X85140 H.sapiens A
30	23.4	57.1	26621	2	AC020878	AC020878 Mus muscu
31	23.4	57.1	39407	2	AC010648	AC010648 Homo sapi
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34	23.4	57.1	144494	9	AC099534	AC099534 Homo sapi
35	23.4	57.1	176291	2	AC023583	AC023583 Homo sapi
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37	23.4	57.1	188810	2	AC115398	AC115398 Rattus no
38	23.4	57.1	203230	2	AC026346	AC026346 Homo sapi
39	23.4	57.1	270000	9	AB026898	AB026898 Homo sapi
40	23.2	56.6	7353	6	AX344975	AX344975 Sequence
41	23.2	56.6	10543	1	AE007241	AE007241 Sinorhizo
42	23.2	56.6	315000	1	RME603644	AL603644 Rhizobium
43	23.2	56.6	315000	1	BC004261	BC004261 Homo sapi
44	23	56.1	1351	9	BC004261	BC004261 Homo sapi
45	23	56.1	1510	9	BC024233	BC024233 Homo sapi

ALIGNMENTS

RESULT 1	AX350512	Sequence 24 from Patent WO0179561.	1350 bp	DNA	linear	PAT 06-FEB-2002
AX350512	LOCUS	AX350512	Sequence 24 from Patent WO0179561.			
	DEFINITION	AX350512				
	ACCESSION	AX350512				
	VERSION	AX350512.1	GI:18616107			
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	SOURCE	Homo sapiens				
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	REFERENCE	1				
	AUTHORS	Liggett, S.B. and Small, K.M.				
	TITLE	Alpha-2 adrenergic receptor polymorphisms				
	JOURNAL	Patent: WO 0179561-A 24 25-Oct-2001;				

Pred. No. is the number of results predicted by chance to have a

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:24:01 ; Search time 48.9583 Seconds
(without alignments)
1885.930 Million cell updates/sec

Title: US-09-636-259C-1_COPY_730_770
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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4	25	61.0	1733 24 ABQ47499 Oligonucleotide fo
5	25	61.0	7353 24 ABL32072 Human immune syste
6	25	61.0	7353 24 AAD28362 Human chemically t
7	24	58.5	36 21 AA294312 Rat cholecystokini
8	24	58.5	37 21 AA294369 Human alpha 2A adr
9	23.4	57.1	14855 22 ABA15164 Human nervous syst

10	23.4	57.1	22028	24	ABA93286	Human acetyl-Coenz
11	23.4	57.1	22028	24	ABA93288	Human acetyl-Coenz
c 12	23.2	56.6	1733	24	ABQ47500	Oligonucleotide fo
c 13	23.2	56.6	1733	24	ABQ47501	Oligonucleotide fo
c 14	23.2	56.6	7353	24	ABL32073	Human immune syste
c 15	23.2	56.6	7353	24	AAD28363	Human chemically t
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c 18	22	53.7	3036	22	AAF44733	Novel protein kina
c 19	22	53.7	4705	23	ABU10758	Drosophila melanog
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21	21.8	53.2	1056	24	ABL88015	DNA polymerase III
22	21.8	53.2	1056	24	ABL88016	DNA polymerase III
23	21.8	53.2	1457	24	ABK52770	cDNA encoding mito
24	21.8	53.2	1550	21	AAF21112	Human low adenosin
25	21.8	53.2	1550	21	AAA34990	Human adenosine re
26	21.8	53.2	3089	21	AAF21113	Human low adenosin
27	21.8	53.2	3089	21	AAA34991	Human adenosine re
c 28	21.6	52.7	8254	22	ABA17475	Human nervous syst
29	21.6	52.7	135	20	AA223654	S. mobaraense tran
30	21.6	52.7	245	20	AA223652	Streptovorticilliu
31	21.6	52.7	1218	13	AAQ24197	Transglutaminase (
32	21.6	52.7	1322	13	AAQ24201	Transglutaminase (
33	21.6	52.7	1809	22	AAH20188	S. mobaraense IFO
34	21.6	52.7	1809	22	AAF86283	DNA encoding prepr
35	21.4	52.2	1436	20	AAK98241	Nucleotide sequenc
36	21.4	52.2	1732	22	AAK52471	Human polynucleoti
37	21.4	52.2	1763	22	AAK51487	Human polynucleoti
c 38	21.4	52.2	2787	19	AAV28914	Rat semaphorin y e
c 39	21.4	52.2	3195	19	AAV28913	Human secreted pro
c 40	21	51.2	344	21	AAK17573	Human cDNA encodin
c 41	21	51.2	514	22	AAS26210	Human DBI/ACBP-li
c 42	21	51.2	1123	19	AAV20912	Human DBI/ACBP-li
c 43	21	51.2	1239	14	AAQ50395	Lignin peroxidase
c 44	21	51.2	1239	14	AAQ61445	Lignin peroxidase
c 45	21	51.2	1337	22	AAI57930	Human polynucleoti

ALIGNMENTS

RESULT 1	
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XX	AA199917;
XX	18-FEB-2002 (first entry)
XX	Human alpha-2AAR encoding DNA.
DE	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW	polymorphic site; allelic variant; cardiovascular disease;
KW	central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW	phosphorylation; inositol phosphate; alpha-2AAR;
XX	GenBank Accession AF281308; chromosome 10; ds.
OS	Homo sapiens.
XX	Key
XX	Location/Qualifiers
FT	1..1353
FT	/*tag= a
FT	/product= "alpha-2AAR"
XX	WO200179561-A2.
PN	
XX	25-OCT-2001.
PD	
XX	
PF	17-APR-2001; 2001WO-US12575.
XX	
PR	17-APR-2000; 2000US-0551744.
PR	10-AUG-2000; 2000US-0636259.
PR	19-OCT-2000; 2000US-0692077.

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XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
SQ
Query Match 100.0%; Score 41; DB 23; Length 1350;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGCAGCGAGCGAGGCCAACGGTCTGGGCCCGGAGCG 41
Db 730 GGGGGCAGCGAGCGAGGCCAACGGTCTGGGCCCGGAGCG 770
RESULT 2
AAI99918
ID AAI99918 standard; DNA; 1350 BP.
XX
XX AAI99918;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human alpha-2AAR variant encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
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XX Homo sapiens.
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FT allele
FT replace(753,C)

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PN XX
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PR 17-APR-2001; 2001WO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
PI
XX
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Disclosure; Page 152; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR variant
CC gene.
XX
XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
SQ
Query Match 96.1%; Score 39.4; DB 23; Length 1350;
Best Local Similarity 97.6%; Pred. No. 0.00018;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGGCAGCGAGCGAGGCCAACGGTCTGGGCCCGGAGCG 41
Db 730 GGGGGCAGCGAGCGAGGCCAACGGTCTGGGCCCGGAGCG 770
RESULT 3
ABQ47498
ID ABQ47498 standard; DNA; 1733 BP.
XX
XX ABQ47498;
AC
XX
XX 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW

```

KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
OS Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-BP10074.
XX 01-SEP-2000; 2000DE-1043826.
XX 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
SQ Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
Query Match 61.0%; Score 25; DB 24; Length 1733;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGCCGACCGTCTGGGCCCCGAGCG 41
DB 990 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 1030
RESULT 4
ABQ47499/c
ID ABQ47499 standard; DNA; 1733 BP.
XX ABQ47499;
XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34090.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

XX Homo sapiens.
OS WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP10074.
XX 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
SQ Sequence 1733 BP; 685 A; 585 C; 211 G; 252 T; 0 other;
Query Match 61.0%; Score 25; DB 24; Length 1733;
Best Local Similarity 75.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGGGGCACCAGCGCCGACCGTCTGGGCCCCGAGCG 41
DB 744 GGGGGTATCGAGCGTAGGTTTAAACGGTTTGGGTTTCGAGCG 704
RESULT 5
ABL32072
ID ABL32072 standard; DNA; 7353 BP.
XX ABL32072;
XX 26-MAR-2002 (first entry)
XX Human immune system associated gene SEQ ID NO: 45.
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

KW gene; ds.
 XX OS Homo sapiens.
 XX PN W0200200928-A2.
 XX PD 03-JAN-2002.
 XX PF 02-JUL-2001; 2001WO-EP07537.
 XX PR 30-JUN-2000; 2000DE-1032529.
 XX PR 01-SEP-2000; 2000DE-1043826.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2002-130909/17.
 XX XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX Claim 1; SEQ ID NO 45; 32bp + Sequence Listing; German.
 XX PS The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
 Query Match 61.0%; Score 25; DB 24; Length 7353;
 Best Local Similarity 75.6%; Pred. No. 13;
 Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 5730 GGGGGTATCGAGCGTAGGTTAACGGTTGGGTTTCGAGCG 5770
 RESULT 6
 AAD28362
 ID AAD28362 standard; DNA; 7353 BP.
 AC AAD28362;
 XX 22-APR-2002 (first entry)
 XX DE Human chemically treated genomic DNA #3.
 XX KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
 KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
 KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
 KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
 KW drug abuse; migraine; ds.
 XX OS Homo sapiens.
 XX PN W0200202809-A2.
 XX PD 10-JAN-2002.
 XX PF 02-JUL-2001; 2001WO-EP07540.
 XX PR 30-JUN-2000; 2000DE-1032529.
 XX PR 01-SEP-2000; 2000DE-1043826.
 XX PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2002-154759/20.
 XX XX Novel nucleic acid useful for diagnosis and therapy of behavioral
 PT disorder, neurological disorder and cancer, comprises a sequence of a
 PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
 PT gene
 XX Claim 1; Page 32-36; 190pp; English.
 XX CC The invention relates to nucleic acids comprising a segment of chemically
 CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
 CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
 CC useful for detecting cytosine methylations. The pretreated DNA is useful
 CC for the diagnosis or therapy of behavioural disorders, neurological
 CC disorders and cancer, in particular major depressive disorder, Tourette's
 CC syndrome, schizophrenia, psychiatric and neurological disorders, human
 CC drug abuse, alcoholism, personality traits, compulsive gambling, smoking,
 CC immunodeficiency virus dementia, migraine, behaviour in patients with
 CC schizophrenia, and suicidal behaviour. The nucleic acid is useful for detecting the methylation
 CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
 CC (SNPs). The present sequence is human chemically treated genomic DNA.
 XX SQ Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
 Query Match 61.0%; Score 25; DB 24; Length 7353;
 Best Local Similarity 75.6%; Pred. No. 13;
 Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 GGGGGCAGCGAGCGAGCGCCCAACGGTCTGGGCCCGGAGCG 41
 Db 5730 GGGGGTATCGAGCGTAGGTTAACGGTTGGGTTTCGAGCG 5770
 RESULT 7
 AA294312/c
 ID AA294312 standard; DNA; 36 BP.
 XX AA294312;
 XX 03-JUL-2000 (first entry)
 XX DE Rat cholecystokinin CCKB receptor PCR primer.
 XX KW G protein coupled receptor; cholecystokinin CCKB receptor;
 KW rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
 KW ss.
 XX OS Rattus sp.
 XX PN W0200012704-A2.
 XX PD 09-MAR-2000.
 XX PF 01-SEP-1999; 99WO-US20011.
 XX PR 01-SEP-1998; 98US-0098704.
 XX PA (PAUS/) PAUSCH M H.
 PA (LAIN/) LAI M.
 PA (SILV/) SILVERMAN S.
 PA (BIRS/) BIRSAN C.
 PA (BAUM/) BAUMBAUCH W.
 PA (TSEN/) TSENG E.
 PA (KAJK/) KAJKOWSKI E M.
 PA (OZEN/) OZENBERGER B A.
 XX Pausch MH, Lai M, Silverman S, Birsan C, Baumbauch W, Tseng E;
 PI Kajokowski EM, Ozenberger BA;
 XX

DR WPI; 2000-246753/21.

XX Novel host cells comprising heterologous G protein-coupled receptor

PT modified to be constitutively active, useful for high throughput

PT screening assays for e.g. drugs, insecticides or nematocides -

XX

PS Example 3; Page 25; 75pp; English.

XX

CC This is the DNA sequence of a primer that was used in the PCR

CC amplification of DNA encoding the N-terminal portion (including 22

CC amino acids proximal to the 5th transmembrane domain) of rat

CC cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR).

CC The PCR product was used in the construction of an intracellular

CC loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion

CC of IC3 of mammalian GPCRs is correlated with improved functional

CC expression in yeast cells with retention of full ability to couple

CC to the heterotrimeric G protein. The invention provides modified

CC GPCRs having a mutation in IC3 that results in an improved functional

CC response in cell-based assays. The modification promotes growth

CC stimulation by a GPCR agonist, especially by improving coupling

CC between the receptor and a heterotrimeric G protein. Polynucleotides

CC encoding the mutated GPCR, chimeric GPCR, vectors and host cells are

CC also claimed. The modified GPCRs can be used in improved high

CC throughput screening assays (especially in yeast cells) for

CC therapeutic drugs, insecticides, nematocides etc.

XX

SQ Sequence 36 BP; 2 A; 15 C; 16 G; 3 T; 0 other;

Query Match 58.5%; Score 24; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCCCAACGGTCTGGGCCCCGAGCG 41

DB 36 GCCCAACGGTCTGGGCCCCGAGCG 13

RESULT 8

AAZ94369/c

ID AAZ94369 standard; DNA; 37 BP.

XX

AC AAZ94369;

XX

DT 03-JUL-2000 (first entry)

XX

DE Human alpha 2A adrenergic receptor PCR primer.

XX

KW G protein coupled receptor; GPCR; human;

XX

KW alpha 2A adrenergic receptor; drug screening; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200012705-A2.

XX

PD 09-MAR-2000.

XX

FF 01-SEP-1999; 99WO-US20013.

XX

PR 01-SEP-1998; 98US-0098704.

XX

PA (PAUSCH) PAUSCH M H.

PA (WESS) WESS J.

XX

PI Pausch MH, Wess J;

XX

DR WPI; 2000-246754/21.

XX

PT New G protein-coupled receptors with a mutation in an intracellular

PT domain, useful for high throughput screening assays for e.g. drugs,

PT insecticides or nematocides -

XX

PS Example 5; Page 16; 37pp; English.

XX

CC This is the DNA sequence of a primer that was used in the PCR

CC amplification of DNA encoding the N-terminal portion (including 39

CC amino acids proximal to the 5th transmembrane domain) of human

CC alpha 2A adrenergic receptor, a G protein coupled receptor (GPCR).

CC The PCR product was used in the construction of an intracellular

CC loop 3 (IC3) deleted receptor mutant. Deletion of a portion

CC of IC3 of mammalian GPCRs is correlated with improved functional

CC expression in yeast cells with retention of full ability to couple

CC to the heterotrimeric G protein. The invention provides modified

CC GPCRs having a mutation in IC3 that results in an improved functional

CC response in cell-based assays. The modification promotes growth

CC stimulation by a GPCR agonist, especially by improving coupling

CC between the receptor and a heterotrimeric G protein. Polynucleotides

CC encoding the mutated GPCR, chimeric GPCR, vectors and host cells are

CC also claimed. The modified GPCRs can be used in improved high

CC throughput screening assays (especially in yeast cells) for

CC therapeutic drugs, insecticides, nematocides etc.

XX

SQ Sequence 37 BP; 2 A; 15 C; 17 G; 3 T; 0 other;

Query Match 58.5%; Score 24; DB 21; Length 37;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCCCAACGGTCTGGGCCCCGAGCG 41

DB 37 GCCCAACGGTCTGGGCCCCGAGCG 14

RESULT 9

ABA15164

ID ABA15164 standard; DNA; 14855 BP.

XX

AC ABA15164;

XX

DT 23-JAN-2002 (first entry)

XX

DE Human nervous system related polynucleotide SEQ ID NO 7495.

XX

KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;

KW antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;

KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX

OS Homo sapiens.

XX

PN WO200159063-A2.

XX

PD 16-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01334.

XX

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225277.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234999.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 17-NOV-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7495; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB114678-AB118001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 14855 BP; 3335 A; 3554 C; 4013 G; 3953 T; 0 other;
 Query Match 57.1%; Score 23.4; DB 22; Length 14855;
 Best Local Similarity 73.2%; Pred. No. 44;
 Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCGCCACCGCTCTGGGCCCCGACG 41
 Db 265 GCGGGCTTCAAGGTGAGGCGCCGAGGCTCTGGGCGCGAGTG 305

RESULT 10

ABA93286
 ID ABA93286 standard; DNA; 22028 BP.

XX ABA93286;

XX 22-APR-2002 (first entry)

XX Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:1.

XX Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
 KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
 KW single nucleotide polymorphism; polymorphic variant; enzyme; gene, ds.
 XX
 OS Homo sapiens.

Key Location/Qualifiers

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 FT FT replace(3637,A)
 FT FT /*tag= b
 FT FT /standard_name= "single nucleotide polymorphism (SNP)"
 FT FT replace(4033,T)
 FT FT /*tag= c
 FT FT /standard_name= "single nucleotide polymorphism (SNP)"
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 FT FT replace(4176,A)
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 FT FT replace(4276,C)
 FT FT /*tag= f
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 FT FT replace(9110,G)
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 FT FT /standard_name= "single nucleotide polymorphism (SNP)"
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XX WO200187903-A2.

XX 22-NOV-2001.

XX 03-MAY-2001; 2001WO-US14330.

XX 18-MAY-2000; 2000US-205022P.

XX (GENA-) GENA1SSANCE PHARM INC.
 PA (DUDA/) DUDA A E.

XX Chew A, Koshy B;

XX WPI; 2002-164134/21.

XX Isolated polynucleotide, comprising a polymorphic variant of the
 CC acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
 CC thiolase) gene useful for providing haplotype information and in
 CC therapy for treating related disorders

XX Claim 19; Fig 1A-I; 93pp; English.

XX The present invention describes a polypeptide (I) which is a polymorphic
 CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal
 CC 3-oxoacyl-Coenzyme A thiolase) ACAA1 protein (AB05516). ACAA1 is located
 CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
 CC where the sequence comprises one of the haplotypes shown in Table 4 or
 CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
 CC given in the specification. The polynucleotide encoding ACAA1 can be used
 CC for providing haplotype and genotype information of an individual.
 CC Furthermore, the polynucleotide is useful for the treatment of disorders
 CC related to its abnormal expression or function. The present sequence
 CC represents the human ACAA1 gene, featuring all the single nucleotide
 CC polymorphisms (SNP) possible, from the present invention.

XX Sequence 22028 BP; 4811 A; 5599 C; 6137 G; 5481 T; 0 other;

Query Match 57.1%; Score 23.4; DB 24; Length 22028;
 Best Local Similarity 73.2%; Pred. No. 44;
 Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCGCCACCGCTCTGGGCCCCGACG 41
 Db 4199 GCGGGCTTCAAGGTGAGGCGCCGAGGCTCTGGGCGCGAGTG 4239

RESULT 11

ABA93288
 ID ABA93288 standard; DNA; 22028 BP.

XX ABA93288;

XX 22-APR-2002 (first entry)

XX Human acetyl-Coenzyme A acyltransferase 1 gene SEQ ID NO:99.

KW Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
KW single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds.
XX
OS Homo sapiens.
XX
FN WO200187903-A2.
XX
PD 22-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14330.
XX
XX 18-MAY-2000; 2000US-205022P.
XX
XX (GENA-) GENAISANCE PHARM INC.
PA (DUDA/) DUDA A E.
XX
XX Chew A, Koshiy B;
PI WPI; 2002-164134/21.
XX
XX Isolated polynucleotide, comprising a polymorphic variant of the
XX acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A
XX thiolase) gene useful for providing haplotype information and in
XX therapy for treating related disorders -
XX
XX Disclosure; Page 85-93; 93pp; English.
XX
XX The present invention describes a polypeptide (I) which is a polymorphic
XX variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal
XX 3-oxoacyl-Coenzyme A thiolase) ACAA1 protein (ABR05516). ACAA1 is located
XX on chromosome 3p23-p22. (I) can be encoded by ABR933286 (or ABR933288)
XX where the sequence comprises one of the haplotypes shown in Table 4 or
XX one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
XX given in the specification. The polynucleotide encoding ACAA1 can be used
XX for providing haplotype and genotype information of an individual.
XX Furthermore, the polynucleotide is useful for the treatment of disorders
XX related to its abnormal expression or function. The present sequence
XX represents the human ACAA1 gene, where all the single nucleotide
XX polymorphisms (SNP) possible have been given in the sequence using the
XX standard ambiguity codes.
XX
XX Sequence 22028 BP; 4808 A; 5592 C; 6133 G; 5476 T; 19 other;
SQ

Query Match 57.1%; Score 23.4; DB 24; Length 22028;
Best Local Similarity 73.2%; Pred. No. 44;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGCCCAACGGTCTGGGCGCGAGCG 41
DB 4199 GCGGCTTCAAGGTGAGGCCCGAGGGTCTGGGCGCGAGTG 4239

RESULT 12
ABQ47500/C
ID ABQ47500 standard; DNA; 1733 BP.
XX
XX ABQ47500;
AC
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS
XX WO200218632-A2.
FN
XX
PD 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EPI0074.
PF
XX

XX
PF 01-SEP-2001; 2001WO-EPI0074.
XX
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX ABQ3410-ABQ3412 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
XX Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
SQ

Query Match 56.6%; Score 23.2; DB 24; Length 1733;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGGAGCGCCCAACGGTCTGGGCGCGAGCG 41
DB 739 CACCGAGCGGAGCGCCCAACGGTCTAAACCGCGAAG 704

RESULT 13
ABQ47501
ID ABQ47501 standard; DNA; 1733 BP.
XX
XX ABQ47501;
AC
XX
XX 12-JUL-2002 (first entry)
DT
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS
XX WO200218632-A2.
FN
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EPI0074.
PF
XX

```

PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
PA (EPiG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 1733;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGGAGCCCAACGGTCTGGGCCCCGAGCG 41
DB 995 CACCGAAGCGAARACCCCAACGATCTAAACCCCGAAG 1030

RESULT 14
ABL32073/c
ID ABL32073 standard; DNA; 7353 BP.
XX
XX ABL32073;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SEQ ID NO: 46.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antihistaminic; antianemic; cytostatic; neurotropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.

Query Match 56.6%; Score 23.2; DB 24; Length 1733;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGGAGCCCAACGGTCTGGGCCCCGAGCG 41
DB 995 CACCGAAGCGAARACCCCAACGATCTAAACCCCGAAG 1030

RESULT 15
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
XX AAD28363;
XX
XX 22-APR-2002 (first entry)
XX
XX Human chemically treated genomic DNA #4.
XX
XX Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1c-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
XX Homo sapiens.
XX
XX WO200202809-A2.
XX
XX 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07540.
XX
XX 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
DR
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation
XX
XX Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis, and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 7353;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CACCGAGCGGAGCCCAACGGTCTGGGCCCCGAGCG 41
DB 1619 CACCGAAGCGAARACCCCAACGATCTAAACCCCGAAG 1584

RESULT 15
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
XX AAD28363;
XX
XX 22-APR-2002 (first entry)
XX
XX Human chemically treated genomic DNA #4.
XX
XX Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1c-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
XX Homo sapiens.
XX
XX WO200202809-A2.
XX
XX 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07540.
XX
XX 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-154759/20.
DR
XX
XX Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1c-receptor
PT gene

```

XX Claim 1; Page 36-40; 190pp; English.
PS
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;

Query Match 56.6%; Score 23.2; DB 24; Length 7353;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 6 CACCGAGCGCAGCCCAACGGTCTGGGCCCGCGAGCG 41
| | | | | | | | | | | | | | | | | | | | | |
Db 1619 CACCGAAGCGCAACCCCAACGATCTAAACCCGGAACG 1584

Search completed: March 10, 2003, 18:59:36
Job time : 56.9583 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:31:11 ; Search time 2.88857 Seconds
(without alignments)
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Title: US-09-636-259C-1_COPY_730_770
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	21.6	52.7	1218	1	US-08-136-993-8
3	21.6	52.7	1322	1	US-08-136-993-12
4	21.4	52.2	1436	4	US-09-199-637A-131
5	21	51.2	1123	1	US-08-700-626-2
6	20.8	50.7	598	4	US-08-998-416-1090
7	20.8	50.7	686	4	US-08-998-416-1040
8	20.6	50.2	35060	3	US-08-814-095-7
9	20.4	49.8	232	6	5318899-25
10	20.4	49.8	294	6	5318899-27
11	20.4	49.8	9775	4	US-08-977-171-1
12	20.4	49.8	9934	4	US-08-977-171-2
13	20.2	49.3	2036	3	US-08-923-454A-17
14	19.8	48.3	51	1	US-07-690-983D-17
15	19.8	48.3	54	1	US-07-690-983D-27
16	19.8	48.3	4190	3	US-08-938-291A-2
17	19.8	48.3	44377	2	US-08-804-198-1
18	19.8	48.3	44377	2	US-08-804-198-1
19	19.8	48.3	4403765	4	US-09-103-840A-2
20	19.8	48.3	4411529	4	US-09-103-840A-1
21	19.6	47.8	1008	4	US-09-091-097-38
22	19.4	47.3	1556	4	US-09-043-937A-3
23	19.4	47.3	33529	4	US-09-144-085-3
24	19.4	47.3	4403765	4	US-09-103-840A-2
25	19.2	46.8	856	1	US-08-117-373-10
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27	19.2	46.8	4724	1	US-08-404-671-3

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	29	19.2	46.8	6763	2	US-08-756-506-23	Sequence 23, Appli
	30	19.2	46.8	8517	3	US-08-827-208-1	Sequence 1, Appli
	31	19.2	46.8	8517	4	US-09-500-358-1	Sequence 1, Appli
	32	19.2	46.8	10807	1	US-08-498-809-1	Sequence 1, Appli
	33	19.2	46.8	10807	1	US-08-206-176-7	Sequence 7, Appli
	34	19.2	46.8	10807	2	US-08-756-506-5	Sequence 5, Appli
	35	19.2	46.8	50937	4	US-09-428-517-1	Sequence 1, Appli
	36	19	46.3	459	2	US-08-387-942C-31	Sequence 31, Appli
	37	19	46.3	3164	1	US-08-188-228-49	Sequence 49, Appli
	38	19	46.3	3164	1	US-08-332-643-43	Sequence 43, Appli
	39	19	46.3	3164	1	US-08-332-638-49	Sequence 49, Appli
	40	19	46.3	6803	3	US-08-665-259-19	Sequence 19, Appli
	41	19	46.3	6803	3	US-08-762-500-19	Sequence 19, Appli
	42	19	46.3	12588	2	US-08-387-942C-1	Sequence 1, Appli
	43	19	46.3	35100	2	US-08-770-379-19	Sequence 19, Appli
	44	19	46.3	35100	4	US-08-757-669A-19	Sequence 19, Appli
	45	19	46.3	35100	4	US-09-230-371A-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1
US-08-136-993-6
; Sequence 6, Application US/08136993
; Patent No. 5420025
; GENERAL INFORMATION:
; APPLICANT: Takagi, Hiroshi
; APPLICANT: Arafuka, Shino
; APPLICANT: Matsui, Hiroshi
; APPLICANT: Washizu, Kinya
; APPLICANT: Ando, Keiichi
; APPLICANT: Koikeda, Satoshi
; TITLE OF INVENTION: Recombinant transglutaminase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,993
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/777,447
; FILING DATE:
; APPLICATION NUMBER: JP 2-282566
; FILING DATE: 19-OCT-1990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-136-993-6

Query Match 52.7%; Score 21.6; DB 1; Length 225;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 GGGGGCAGCGCCAGCGCCCAACGGTCTGGGCCCC 36
Db 189 GGCCGCTTCGAGCGCGCGCCGCTGTTCCGGGCCCC 224

RESULT 2
US-08-136-993-8
; Sequence 8, Application US/08136993
; Patent No. 5420025
; GENERAL INFORMATION:
; APPLICANT: Takagi, Hiroshi
; APPLICANT: Arafuka, Shino
; APPLICANT: Matsui, Hiroshi
; APPLICANT: Washizu, Kinya
; APPLICANT: Ando, Keiichi
; APPLICANT: Koikeda, Satoshi
; TITLE OF INVENTION: Recombinant transglutaminase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,993
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/777,447
; FILING DATE:
; APPLICATION NUMBER: JP 2-282566
; FILING DATE: 19-OCT-1990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptovorticillum sp.
; IMMEDIATE SOURCE:
; CLONE: pTV118 NcoI
; US-08-136-993-8

Query Match 52.7%; Score 21.6; DB 1; Length 1218;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGCGAGCGCCCAACGGTCTGGGCCCC 36
Db 189 GGCCGCTTCGAGCGCGCGCCGCTGTTCCGGGCCCC 224

RESULT 3
US-08-136-993-12
; Sequence 12, Application US/08136993
; Patent No. 5420025
; GENERAL INFORMATION:
; APPLICANT: Takagi, Hiroshi
; APPLICANT: Arafuka, Shino
; APPLICANT: Matsui, Hiroshi
; APPLICANT: Washizu, Kinya
; APPLICANT: Ando, Keiichi
; APPLICANT: Koikeda, Satoshi
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1436

Query Match 52.7%; Score 21.6; DB 1; Length 1322;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGCGCCCAACGGTCTGGGCCCC 36
Db 282 GGCCGCTTCGAGCGCGCGCCGCTGTTCCGGGCCCC 317

RESULT 4
US-09-199-637A-131
; Sequence 131, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard W.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1436
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-131

Query Match      52.2%; Score 21.4; DB 4; Length 1436;
Best Local Similarity 80.6%; Pred. No. 47;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGGCACCAGCGCAGGCCCAACGGTCTGGGC 33
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Db 1187 GGGCGCCGAGCGCAGCAGCAACCGCTGGC 1217

RESULT 5
US-08-700-626-2/c
; Sequence 2, Application US/08700626
; Patent No. 5734038
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08700,626
; APPLICATION NUMBER: US/08700,626
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0115 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1123 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGANNOT01
; CLONE: 620984
; US-08-700-626-2

Query Match      51.2%; Score 21; DB 1; Length 1123;
Best Local Similarity 73.0%; Pred. No. 64;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 GGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGC 40
    ||| ||| ||||| ||||| |||||
Db 58 GGCTTGGAGGCTGGCCCCACCAGTCTGGTCTGCGAGC 22

RESULT 6
US-08-598-416-1090
; Sequence 1090, Application US/089998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer

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; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1040:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1635UP
; US-08-998-416-1040

Query Match 50.78; Score 20.8; DB 4; Length 686;
Best Local Similarity 70.08; Pred. No. 75;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGAGCGCCCAACGGTCTGGGCCCGCAGC 40
   |||||
Db 233 GCGAGCACCAGCGCGCTGGCCCAACAGGCTCGACAGCGAGC 272

RESULT 8
US-08-814-095-7
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE"
; DESCRIPTION: promotor, ACHE gene and ARS gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:
; NAME/KEY: promotor
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 22465..22537
; OTHER INFORMATION: /function= "non-translated"
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 24090..25177
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "(translation start:
; OTHER INFORMATION: 24110)"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25524..26009
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27005..27274
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27255..28007
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 5
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 27385..27387
; FEATURE:
; NAME/KEY: exon
; LOCATION: 28008..28129
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 6
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 28129..28131
; FEATURE:
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NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance"
OTHER INFORMATION: gene
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: exon
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
FEATURE:
NAME/KEY: exon
LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
FEATURE:
NAME/KEY: exon
LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
FEATURE:
NAME/KEY: exon
LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
FEATURE:
NAME/KEY: exon
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
FEATURE:
NAME/KEY: exon
LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
FEATURE:
NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FEATURE:
NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
FEATURE:
NAME/KEY: exon
LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
FEATURE:
NAME/KEY: exon

LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
FEATURE:
NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
Query Match 50.2%; Score 20.6; DB 3; Length 35060;
Best Local Similarity 74.3%; Pred. No. 79;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2 GGGCACCAGCGCAGGCCCAACGGTCTGGGCCCC 36
|||||
Db 22583 GGGCACCAGCGCTCCCGAGGGTCCAGGCCCC 22617
RESULT 9
5318899-25/c
; Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.; WOLF, DAVID L.; CHARO,
; ISRAEL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-OCT-1989
; APPLICATION NUMBER: 367,509
; FILING DATE: 16-JUN-1989
; SEQ ID NO: 25:
; LENGTH: 232
5318899-25
Query Match 49.8%; Score 20.4; DB 6; Length 232;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 4 GGCACCAGCGCAGGCCCAACGGTCTGGGCCCGAGCG 41
|||||
Db 124 GGCACATCACAGCACAGACCGTCTGCCACTGAGCG 87
RESULT 10
5318899-27/c
; Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.; WOLF, DAVID L.; CHARO,
; ISRAEL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-OCT-1989
; APPLICATION NUMBER: 367,509
; FILING DATE: 16-JUN-1989
; SEQ ID NO: 27:
; LENGTH: 294
5318899-27
Query Match 49.8%; Score 20.4; DB 6; Length 294;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 4 GGCACCAGCGCAGGCCCAACGGTCTGGGCCCGAGCG 41
|||||
Db 186 GGCACATCACAGCACAGACCGTCTGCCACTGAGCG 149

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RESULT 11
US-08-977-171-1/c
; Sequence 1, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6232112west Center, 90 South 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,171
; FILING DATE: 24-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 10552.13US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9775 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-977-171-1
;
; Query Match 49.8%; Score 20.4; DB 4; Length 9775;
; Best Local Similarity 71.1%; Pred. No. 95;
; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
;
; QY 3 GGGCACCAGCGCAGGCCAACGGTCTGGGCCCGGAGC 40
; | | | | | | | | | | | | | | | | | | | | | | | |
; Db 2547 GGGCACCAGCGCAGGCCAACGGTCTGGGCCCGGAGC 2510
;
; RESULT 12
US-08-977-171-2/c
; Sequence 2, Application US/08977171
; Patent No. 6232112
; GENERAL INFORMATION:
; APPLICANT: CATCHESIDE, DAVID E.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
; TITLE OF INVENTION: OF DNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6232112west Center, 90 South 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,171
; FILING DATE: 24-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 10552.13US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9934 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-977-171-2
;
; Query Match 49.8%; Score 20.4; DB 4; Length 9934;
; Best Local Similarity 71.1%; Pred. No. 95;
; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
;
; QY 3 GGGCACCAGCGCAGGCCAACGGTCTGGGCCCGGAGC 40
; | | | | | | | | | | | | | | | | | | | | | | | |
; Db 2651 GGGCACCAGCGCAGGCCAACGGTCTGGGCCCGGAGC 2614
;
; RESULT 13
US-08-923-454A-17/c
; Sequence 17, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livi, George
; APPLICANT: Karran, Eric
; APPLICANT: Clinkenbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
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```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2036 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: Feature polymorphism at 1325
;
US-08-923-454A-17

Query Match 49.3%; Score 20.2; DB 3; Length 2036;
Best Local Similarity 68.3%; Pred. No. 1.1e+02;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GCGGGCAGCGCGCCGCTCTGGGCGCCGAGCG 41
Db 190 GCGGGCAGCGCGCCGCTCTGGGCGCCGAGCG 150

RESULT 14
US-07-690-983D-17
; Sequence 17, Application US/07690983D
; Patent No. 5403586
; GENERAL INFORMATION:
; APPLICANT: RUSSELL-JONES, Gregory J.
; APPLICANT: STEWART, Andrew G.
; APPLICANT: TSONIS, Con G.
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU90/00373
; FILING DATE: 24-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/148 CHAC
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA
; IMMEDIATE SOURCE:
; CLONE: pBTA 735
; FEATURE:

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2036 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: Feature polymorphism at 1325
;
US-08-923-454A-17

Query Match 48.2%; Score 19.8; DB 1; Length 51;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 GGGCAGCGAGCGCGCCCAACGGTCTGGGCGCCGAGCG 41
Db 3 GGGCGGAGCGACTGGTCATATGGTCTGCGCGGGG 41

RESULT 15
US-07-690-983D-27
; Sequence 27, Application US/07690983D
; Patent No. 5403586
; GENERAL INFORMATION:
; APPLICANT: RUSSELL-JONES, Gregory J.
; APPLICANT: STEWART, Andrew G.
; APPLICANT: TSONIS, Con G.
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU90/00373
; FILING DATE: 24-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/148 CHAC
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA
; IMMEDIATE SOURCE:
; CLONE: pBTA 740
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..54
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13..42
; OTHER INFORMATION: /note= "Coding sequence for LHRH
; OTHER INFORMATION: analogue"
;
US-07-690-983D-27
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Query Match 48.3%; Score 19.8; DB 1; Length 54;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 3 GGGCACCAGCGCAGGCCCAACGGTCTGGGCCCGGAGCG 41
Db 6 GGGCCCCGAGCACTGGTTCATATGGTCTGGGTCCCGGGG 44

Search completed: March 11, 2003, 07:41:04
Job time : 20.8886 secs


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; APPLICANT: MOMOSE, HARUO
; TITLE OF INVENTION: A METHOD OF PRODUCING MICROBIAL TRANSLUTAMINASE
; FILE REFERENCE: 220567USOCONT
; CURRENT APPLICATION NUMBER: US/10/124,429
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/JP00/07135
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: JP 11-295649
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Streptovorticillum mobaraense
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578)..(1798)
; OTHER INFORMATION:
US-10-124-429-3

Query Match      52.7%; Score 21.6; DB 9; Length 1809;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGGGCGACCGAGCGCAGCCCAACGGTCTGGGCCCC 36
Db 769 GCGCGCTTCGAGCGCGCGCCGCTGCTTCGGGCCCC 804

RESULT 3
US-09-975-719-131
; Sequence 131, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Rahme, Laurence G.
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361003
; CURRENT APPLICATION NUMBER: US/09/975,719
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/199,637
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-975-719-131

Query Match      52.2%; Score 21.4; DB 9; Length 1436;
Best Local Similarity 80.6%; Pred. No. 52;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGGCGCCGAGCGCAGCCCAACGGTCTGGGC 33
Db 1187 GGGCGCCGAGCGCAGCAGCAACCGCTGGC 1217

RESULT 4
US-09-764-864-389/c
; Sequence 389, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 389
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-389

Query Match      51.2%; Score 21; DB 10; Length 514;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 5 GCACCGAGCGCAGCGCCCAACGGTCTGGGCCCCGAGCG 41
Db 453 GCACCGAGTGCCAGGACATCGAGCTGTGCCCGAGTG 417

RESULT 5
US-09-867-550-1483
; Sequence 1483, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and f
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1483
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1483

Query Match      51.2%; Score 21; DB 10; Length 569;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGCGACCGAGCGCAGCGCCCAACGGTCTGGGCCCCG 37
Db 462 GGAGCCACCGAGCTTGGGGCCATCATCTGGGCGCTG 498

RESULT 6
US-09-859-101-2/c
; Sequence 2, Application US/09859101
; Patent No. US2002006825A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (344)..(1192)
US-10-098-841-134

Query Match 51.2%; Score 21; DB 9; Length 1337;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GGCACCGAGCGCAGCCCAACGGTCTGGGCCCGCAGC 40
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 GGCCTGGAGGCTGGCCCAACGAGTCTGGTGGCGAGC 245

RESULT 8
US-09-864-761-5736/c
; Sequence 5736, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5736
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1

; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,101
; FILING DATE: 14-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,626
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0115 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1123 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGANNOT01
; CLONE: 620984
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-859-101-2

Query Match 51.2%; Score 21; DB 10; Length 1123;
Best Local Similarity 73.0%; Pred. No. 71;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GGCACCGAGCGCAGCCCAACGGTCTGGGCCCGCAGC 40
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 GGCCTGGAGGCTGGCCCAACGAGTCTGGTGGCGAGC 22

RESULT 7
US-10-098-841-134/c
; Sequence 134, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes version 1.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: DNA

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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
US-09-864-761-5736

Query Match 50.7%; Score 20.8; DB 10; Length 457;
Best Local Similarity 70.0%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGCGCCGAGCGAGCCCAACGGTCTGGGCCCGGAGC 40
Db 188 GCGGCCCCGGCGGAGGCCACGTGAGGTCCAGGAAC 149

RESULT 9

US-10-006-950-1
; Sequence 1, Application US/10006950
; Patent No. US20020161216A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Bonini, James A.
; TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF4 RECEPTOR
; FILE REFERENCE: 58799
; CURRENT APPLICATION NUMBER: US/10/006,950
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: US/09/266,407
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-950-1

Query Match 50.7%; Score 20.8; DB 9; Length 1461;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGCGCCGAGCGAGCCCAACGGTCTGGGCCCGGAGC 40
Db 1410 GCGGCCCCGGCGGAGGCCACGTGAGGTCCAGGAAC 1449

RESULT 10

US-09-805-467A-3
; Sequence 3, Application US/09805467A
; Patent No. US20020058259A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human Lipoxin A4
; TITLE OF INVENTION: Receptor-Like Protein
; FILE REFERENCE: 4974.00453
; CURRENT APPLICATION NUMBER: US/09/805,467A
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,037
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-805-467A-3

Query Match 50.7%; Score 20.8; DB 10; Length 2300;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGGCGCCGAGCGAGCCCAACGGTCTGGGCCCGGAGC 40
Db 1980 GCGGCCCCGGCGGAGGCCACGTGAGGTCCAGGAAC 2019

RESULT 11

US-09-819-104A-3/c
; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7521)
US-09-819-104A-3

Query Match 50.7%; Score 20.8; DB 9; Length 7521;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGCGCCGAGCGAGCCCAACGGTCTGGGCCCGGAGC 41
Db 4577 GCGTACCAGCTCAGGCACAATGACCGGGCGCGCGC 4538

RESULT 12

US-09-819-104A-1/c
; Sequence 1, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Query Match 50.7%; Score 20.8; DB 9; Length 8686;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 GGGGCGCCGAGCGAGCCCAACGGTCTGGGCCCGGAGC 41
Db 4733 GCGTACCAGCTCAGGCACAATGACCGGGCGCGCGC 4694

RESULT 13

OTHER INFORMATION: human genomic region containing *ltrpc5*
OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1)
OTHER INFORMATION: containing KvLQT1 gene)

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:30:36 ; Search time 23887.5 Seconds
(without alignments)
915.286 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
Sequence: 1 atgggcctcctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
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- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_ges:*
- 18: em_ges_hum:*
- 19: em_ges_inv:*
- 20: em_ges_pln:*
- 21: em_ges_vrt:*
- 22: em_ges_fun:*
- 23: em_ges_mam:*
- 24: em_ges_mus:*
- 25: em_ges_other:*
- 26: em_ges_pro:*
- 27: em_ges_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	561	41.6	561	14	BM967248
C 2	490.4	36.3	492	14	BM967243
C 3	479	35.5	691	10	BB643669
C 4	453	33.6	453	14	BQ129312
C 5	410.6	30.4	893	13	B1459381
C 6	395	29.3	740	13	B1838282

7	364.8	27.0	1077	9	AL544609	AL544609
8	320.2	23.7	855	17	GGAA2AAR	AL606540 Chicken a
c 9	319.4	23.7	358	13	BM352981	BM352981 ig69h02.y
10	317.6	23.5	867	9	AL530418	AL530418 AL530418
11	317.4	23.5	988	14	BQ887729	BQ887729 AGENCOURT
12	272.6	20.2	297	14	BQ302172	BQ302172 QVO-BT026
13	255.2	18.9	935	14	BQ923710	BQ923710 AGENCOURT
14	226.4	16.8	896	17	CNS03BQW	AL236849 Tetraodon
15	214.6	15.9	966	17	CNS02NV2	AL205895 Tetraodon
c 16	199.8	14.8	1135	9	AL544577	AL544577 AL544577
c 17	197	14.6	805	17	CNS03CEL	AL237702 Tetraodon
18	194.2	14.4	350	10	BE648878	BE648878 UI-M-BH2..
19	185.8	13.8	777	17	LREA2AR	AL606561 Lamprey a
20	185.6	13.7	801	17	GGAA2CAR	AL606541 Chicken a
21	179.4	13.3	1010	17	CNS04CMQ	AL284651 Tetraodon
22	177.2	13.1	702	13	B1836679	B1836679 603089610
23	176.6	13.1	975	17	CNS039RV	AL234232 Tetraodon
24	175.8	13.0	921	17	CCLA2BAR	AL606559 Herring a
25	173.4	12.8	691	17	HIPAA2AR	AL606565 Sea Horse
26	172.6	12.8	774	17	AGAA2C2AR	AL606580 Toothcarp
27	172.4	12.8	882	17	HIPAA2C2AR	AL606568 Sea Horse
28	171.4	12.7	697	17	RESA2AR	AL606551 Frog alph
29	170.6	12.6	2146	11	AK018378	AK018378 Mus muscu
30	169.6	12.6	872	17	ECRA2BAR	AL606560 Horse alp
31	167.8	12.4	825	17	ARUA2BAR	AL606576 Sturgeon
c 32	166.8	12.4	890	17	CNS02WK9	AL217170 Tetraodon
33	164.8	12.2	693	17	ARUA2AAR	AL606574 Sturgeon
34	164	12.1	535	13	BM647571	BM647571 170006873
35	163.4	12.1	723	17	AGAA2A2AR	AL606581 Toothcarp
36	161.8	12.0	829	9	AL549866	AL549866 AL549866
37	160.6	11.9	705	17	HGRA2AAR	AL606570 Shark alp
38	160	11.9	753	17	SCAA2CAR	AL606564 Ostrich a
39	159.4	11.8	788	17	DREA2CAR	AL606584 Zebrafish
40	158.6	11.7	699	17	LOSA2AR	AL606553 Gar alpha
41	154.4	11.4	981	17	HIPAA2BAR	AL606569 Sea Horse
c 42	151.4	11.2	872	9	AL573897	AL573897 AL573897
43	151	11.2	860	17	CNS03HKQ	AL244403 Tetraodon
44	148.8	11.0	780	17	CCLA2CAR	AL606557 Herring a
45	148	11.0	984	9	AL550664	AL550664 AL550664

ALIGNMENTS

RESULT 1
BM967248/c
LOCUS
DEFINITION
i32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION
BM967248
VERSION
BM967248.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Matra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
Other ESTs: i32d04.x1

TITLE
JOURNAL
COMMENT
Endocrine Pancreas Consortium
Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
1. .561
/organism="Homo sapiens"
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/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

63 a 215 c 210 g 73 t

BASE COUNT
ORIGIN

Query Match 41.6%; Score 561; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.8e-92;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 610 TCCTTCTTCGCTCCGCTCATCATGATCTGTCTACGTGGCATCTACCGATGCC 669
Db 561 TCCTTCTTCGCTCCGCTCATCATGATCTGTCTACGTGGCATCTACCGATGCC 502
Qy 670 AAGCGTCGACCGCGTGCACCGCGCGGGTTCGGACGCCGTCGCGCGCGCG 729
Db 501 AAGCGTCGACCGCGTGCACCGCGCGGGTTCGGACGCCGTCGCGCGCGCG 442
Qy 730 GGGGGCACCGAGCGAGGCCCAACGGTCTGGGCCCCGAGCGAGCGCGCGGGGG 789
Db 441 GGGGGCACCGAGCGAGGCCCAACGGTCTGGGCCCCGAGCGAGCGCGGGGG 382
Qy 790 GCAGAGCGCGAACCGCTGCCACCGAGTCAACGGCGCCCTGGCAGCGCGCGGG 849
Db 381 GCAGAGCGCGAACCGCTGCCACCGAGTCAACGGCGCCCTGGCAGCGCGGG 322
Qy 850 GGGCGCGCGACCGAGCGCGCTGGACTGGAGGAGAGCTGCTTCCGACCGCGCG 909
Db 321 GGGCGCGCGACCGAGCGCGCTGGACTGGAGGAGAGCTGCTTCCGACCGCGCG 262
Qy 910 CGGCTTCAGGGCCCCGAGACCGCGCGGTCCCCGGGGCAAGCAAGGCCCGAGCG 969
Db 261 CGGCTTCAGGGCCCCGAGACCGCGCGGTCCCCGGGGCAAGCAAGGCCCGAGCG 202
Qy 970 AGCAGGTGAACCGGGCGACAGCTGCCGGCGCGGGCGGGGGCGAGCGGGATCGG 1029
Db 201 AGCAGGTGAACCGGGCGACAGCTGCCGGCGCGGGCGGGGGCGAGCGGGATCGG 142
Qy 1030 ACGCGCGTGCAGGGCGGGGAGAGCGGTTCGGGGCTGCCAAGGCGTTCGCGTGGCG 1089
Db 141 ACGCGCGTGCAGGGCGGGGAGAGCGGTTCGGGGCTGCCAAGGCGTTCGCGTGGCG 82
Qy 1090 GGGCGGCAACCGCGAGAACGGCTTCACGTTCTGTCGGCCGTGTCATCGGAGTGTTC 1149

Db 81 GGGCGGCAACCGCGAGAACGGCTTCACGTTCTGTCGGCGGTGTCATCGGAGTGTTC 22
Qy 1150 GTGGTGTGCTGGTTCCTCCCTTC 1170
Db 21 GTGGTGTGCTGGTTCCTCCCTTC 1

RESULT 2
BM967243/C
LOCUS BM967243 492 bp mRNA linear EST 29-APR-2002
DEFINITION i32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.
ACCESSION BM967243
VERSION BM967243.1 GI:19561038
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
REFERENCE Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: i32c09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. .492
/organism="Homo sapiens"
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/clone="IMAGE:6136336"
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/sex="Both"
/tissue_type="Islets of Langerhans"
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/lab_host="DH10B"

44 a 202 c 182 g 64 t

BASE COUNT
ORIGIN

[illegible]

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Qy 241 CTGCTGGCCAGCGCTCGTCATCCCTTTCTCGCTGGCCCAACGAGGTTCATGGGCTACTGTGTAC 300
Db 386 CTGCTGGCCAGCGCTGGTCATTCCTTTCTTTTGGCCCAACGAGGTTCATGGGTTACTGTGTAC 327
Qy 301 TTGGCCAAAGGCTTGGTGGGATCTACTCGCGCTCGACGTGCTCTTCTTCGACGTGCTCC 360
Db 326 TTTGGTAAGGTGTGTGTGAGATCTATTGGCTCTCGACGTGCTCTTTTTCGACGTGCTCC 267
Qy 361 ATCGTGACCTGTGGCCATCAGCTGGACGCTACTGTGCTGCTCATCATCACAGGCGCATCGAG 420
Db 266 ATAGTGACCTGTGGCCATCAGCTTTGACCGGTACTGTGCTCATCATCACAGGCGCATCGAG 207
Qy 421 TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCCGTGTGGGTATC 480
Db 206 TACAACCTGAAGCGCACGCGCGCTCGCATCAAGGCCATCATTTGTCACCGTGTGGGTATC 147
Qy 481 TCGGCGCGTCACTCTCTTCCGCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGGC 540
Db 146 TCGGCTGTCACTCTCTTCCGCGCACTCATCTCCATAGAGAAGAGGCGCTGGCGCGG 87
Qy 541 CCGCAGCGCGCGAGCGCGCTGCGAGATCAACGACGAGAGTGTGATCTATCTCGTCG 600
Db 86 CAGCAGCGCGCGAGCGCAAGCTGCAAGATCAACGACGAGAAGTGTGTATGTATCTCTCTCG 27
Qy 601 TGCATCGGCTCTTCTTCGCTCCCT 625
Db 26 TCCATCGGTTCTTCTTCGCGCCTT 2

RESULT 4
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LOCUS BQ129312 453 bp mRNA linear EST 29-APR-2002
DEFINITION i334d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6136736 5', similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION BQ129312
VERSION BQ129312.1 GI:20203223
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Melton,D., Brown,J., Keny,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,D., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: i334d05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .453
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6136736"

FEATURES
source
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/sex="Both"
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/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaïdo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT 41 a 189 c 164 g 59 t
ORIGIN
Query Match 33.6%; Score 453; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.le-72;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 718 GCGCGCGCGCGGGGGCACCGAGCGAGGCCCAACGGTCTGGGCCCCCGAGCGAGCGCG 777
Db 453 GCGCGCGCGCGGGGGCACCGAGCGAGGCCCAACGGTCTGGGCCCCCGAGCGAGCGCG 394
Qy 778 GCGCGCGGGGGCGCAGAGCGCGCAACCGCTGCCACCCAGCTCAACGGCGCCCTTGGCGAG 837
Db 393 GCGCGCGGGGGCGCAGAGCGCGCAACCGCTGCCACCCAGCTCAACGGCGCCCTTGGCGAG 334
Qy 838 CCGCGCGCGCGCGCGCGCGCGCACACCGCGCTGACCTGGAGGAGAGCTCTCTTCC 897
Db 333 CCGCGCGCGCGCGCGCGCGCGCACACCGCGCTGACCTGGAGGAGAGCTCTCTTCC 274
Qy 898 GACCACGCGAGCGGCGCTCCAGAGCGCGCGCACGCCGCGCTCCCGGGGCAAGGC 957
Db 273 GACCACGCGAGCGGCGCTCCAGAGCGCGCGCACGCCGCGCTCCCGGGGCAAGGC 214
Qy 958 AAGGCCCGAGCGAGCGAGCTGAAGCGCGGGCGACAGCTTCCGCGCGCGCGCGCGGGGCG 1017
Db 213 AAGGCCCGAGCGAGCGAGCTGAAGCGCGGGCGACAGCTTCCGCGCGCGCGCGGGGCG 154
Qy 1018 ACGGGGATCGGGACCGCGCGCTGACGGGCGGGGAGGAGCGCGTCCGGGCTGCCAAGGC 1077
Db 153 ACGGGGATCGGGACCGCGCGCTGACGGGCGGGGAGGAGCGCGTCCGGGCTGCCAAGGC 94
Qy 1078 TCGCGCTGGCGGGCGCGCAGAACCGCGAGAACGCGCTTACGTTCTGCTGGCGCTGTGC 1137
Db 93 TCGCGCTGGCGGGCGCGCAGAACCGCGAGAACGCGTTCACGTTCTGCTGGCGCTGTGC 34
Qy 1138 ATCGGAGTGTTCGTGGTGTGCTGTGTTCCCTTC 1170
Db 33 ATCGGAGTGTTCGTGGTGTGCTGTGTTCCCTTC 1
RESULT 5
BQ1459381
LOCUS BQ1459381 893 bp mRNA linear EST 21-AUG-2001
DEFINITION 603200147P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5',
BQ1459381 mRNA sequence.
ACCESSION BQ1459381
VERSION BQ1459381.1 GI:15250037
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
```


TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGR1), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11671 row: m column: 11
High quality sequence stop: 716.

FEATURES

source

1. 893
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/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcggg
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGR1, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 149 a 303 c 290 g 151 t

Query Match 30.4%; Score 410.6; DB 13; Length 893;

Best Local Similarity 86.0%; Pred. No. 6.1e-65;

Matches 586; Conservative 0; Mismatches 74; Indels 21; Gaps 11;

Qy 1 ATGGGCTCCCTGACGCGGACCGGCAACGGAGCTGGAACGGACCGGCGCGGGG 60

Db 213 ATGGGCTCCCTGACGCGGACCGGCAACGGAGCTGGAACGGACCGGCGCGGG 272

Qy 61 GGGCGGCGCGGGCCACCCCTTACTCCCTGACAGGTGACGCTGAGCTGGTGTGCTGGCC 120

Db 273 GGGCGGCGCGGGCCACCCCTTACTCCCTGACAGGTGACGCTGAGCTGGTGTGCTGGCC 332

Qy 121 GGCTCTCATGCTGCTACCGTGTTCGGCAACGCTGCTGCTATCATCGCGGTTCAG 180

Db 333 GGCTCTCATGCTGCTACCGTGTTCGGCAACGCTGCTGCTATCATCGCGGTTCAG 392

Qy 181 AGCGCGCGCTCAAGCGCGCCCAAAACCTTCTTCCTGGTGTCTCTGG--CCTCGGCGGACA 238

Db 393 AGCGCGCGCTCAAGCGCGCCCAAAACCTTCTTCCTGGTGTCTCTGGACCTCGGACGAAAT 452

Qy 239 TCTGTGGCGACGCTCGT-CAATCCCTTTCCTGCTGGCCAAAGAGTCAATGGCTACTGG 297

Db 453 TCTGTGGCGACGCTCGTACATCCCTTTCCTGCTGGCCAAAGAGTCAATGGCTACTGG 512

Qy 298 TACTTCGGCAA--GGCTTGTGGG--AGATCTACTGCGGCTCGACGTCTTCTGCAGT 355

Db 513 TACTTCGGCAAAGGCTTGTGTGGGAATCTACTTGGCGCTCGACGTGCTTCTGCAGT 572

Qy 356 -GCTCCATCGTGACCTGTGCGGCATCAGCTGGACCGCTACTTGGTCCATCACAGGCG 414

Db 573 ACGTCCATCGTGACCTGTGCGGCATCAGCTGGACCGCTACTTGGTCCATCACAGGCG 632

Qy 415 ATGAGTAAACCTGAAGCGACGCGCGCCGATCAAGGCCATCATCATCAACCGTGTGG 474

Db 633 ATGAGTAAACCTGAAGCGACGCGCGCCGATCAAGGCCATCATCATCAACCGTGTGG 692

Qy 475 GTC-ATCTCGGCGGTATCTCTTCCG-----CCGCTCATCTCCATCGAGAGAGG 526

Db 693 GTCATCTCGGCGGTATCTCTTCCGCGGTTTCATCTCCACTCGGAGAACACGCGG 752

Qy 527 GCGCGCGCGCGGGCCC-GCAGCGCGCGGACCGCGCTGCGAGATCAACGA--CCAGAAGT 583

Db 753 CGGACGAGCGCGGCCAGGAAGCGGCCGCGCGGGAAGATCAGCAGCAGAAAGG 812

Qy 584 GGTACGTATCTGCTCGTG--CATCGGCTCTTCTTCGCTCCCTGCTCATCATATCC 640

Db 813 GGTACGTAATTTGAGATCGTGAATGATGACTTTTGTTCGCTCCCTGCTCATCAGAGTCC 872

Qy 641 TGGTCTACGTGCGCATCTACC 661

Db 873 TGG-CAACGCGCGCATATACC 992

RESULT 6

BI838282

LOCUS

DEFINITION BI838282 740 bp mRNA linear EST 04-OCT-2001
603083213F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:522475 5',
mRNA sequence.

ACCESSION BI838282

VERSION BI838282.1

KEYWORDS GI:15949832

SOURCE EST.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 740) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11559 row: i column: 04

High quality sequence stop: 740.

FEATURES

source

1. 740

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/db_xref="taxon:9606"

/clone="IMAGE:522475"

/clone_lib="NIH_MGC_120"

/lab_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector:

PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of spleen and pancreas from 28 yo

male. Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.5 kb, insert size range 1-2.5 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 115 a 240 c 235 g 150 t

ORIGIN

Query Match 29.3%; Score 395; DB 13; Length 740;

Best Local Similarity 100.0%; Pred. No. 4e-62;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 GCAAGGCCGACGAGCGAGGTGAAGCCGGCGGACAGCTCCCGCGCGCGCGGGG 1015

Db 1 GCAAGGCCGACGAGCGAGGTGAAGCCGGCGGACAGCTCCCGCGCGCGGGG 60

Qy 1016 CGACGGGATCGGACCCCGCTGACGGCGCGGGGAGGAGCGCTCGGGCTGCCAAGG 1075

Db 61 CGACGGGATCGGACCCCGCTGACGGCGCGGGGAGGAGCGCTCGGGCTGCCAAGG 120

Qy 1076 CGTCGCGCTGCGCGCGCGGACGAGAACCGGAGAGCGCTTTCACGTTCTGCTCGCGCTGG 1135

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Db 121 CGTCGGCTCGCGCGCGCAGAACCGGAGAACGCTTTCACGTTCTGCTGGCGCTGG 180
Qy 1136 TCATCGGAGTTCGTGGTGTGCTGGTTCCTTCTTCCATACAGCTCACGGCCG 1195
Db 181 TCATCGGAGTTCGTGGTGTGCTGGTTCCTTCTTCCATACAGCTCACGGCCG 240
Qy 1196 TCGGGTCTCGCTGCCAGCAGCAGCTCTTCAAAATCTTCTTCTGGTTCGCTACTGCAACA 1255
Db 241 TCGGGTCTCGCTGCCAGCAGCAGCTCTTCAAAATCTTCTTCTGGTTCGCTACTGCAACA 300
Qy 1256 GTCCTGTAACCGGTTCATCAGCATCTTCAACACAGATTTCCGCGCGCTTCAAGA 1315
Db 301 GCTCGTTGAACCGGTTCATCAGCATCTTCAACACAGATTTCCGCGCGCTTCAAGA 360
Qy 1316 AGATCTCTCTCGGGGAGCAGGAGCGGATCGTG 1350
Db 361 AGATCTCTCTCGGGGAGCAGGAGCGGATCGTG 395

RESULT 7
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LOCUS AL544609 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI021YC24 5
DEFINITION prime, mRNA sequence.
ACCESSION AL544609
VERSION AL544609.1 GI:12877089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 124 a 397 c 385 g 168 t 3 others
ORIGIN
Query Match 27.0%; Score 364.8; DB 9; Length 1077;
Best Local Similarity 75.1%; Pred. No. 1.3e-56;
Matches 500; Conservative 0; Mismatches 152; Indels 14; Gaps 3;

Qy 64 GCGCGCGCGCGCCCTTACTCCTGACGTGACGTGGTGTGCTGGCGCGC 123
Db 360 GGGCGCGCGCGCGAGTTACTCGCGCGCGCGGTGGAGCGGTGGTTCGGTGGGC 419
Qy 124 CTGCTCATGCTGCTCACCGTGTTCGGAACGTGCTGCTCATATCGCGCGGTTCACGAGC 183
Db 420 TTCCTCATGCTTTCACCGTGTGGCAACGTGCTGTTGGTGTATCGCGGTGCTGACCCAGC 479
Qy 184 CGCGCGCTCAAGGGCGCCCAAAACCTCTTCTGCTGTGCTTCTGGCTCGCGCGACATCTG 243
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Db 480 CGGCGCT-GCGCGCGCAGAACCTTCTCTGGTGTGCTGGCTCGCGGACATCCTG 538
Qy 244 GTGCGCACGCTCGTCATCCCTTTCTCGCTGGCCAAAGAGGTCTATGGCTACTGGTACTTC 303
Db 539 GTGCGCACGCTGGTTCATGCCCTTCTCGTTGGCCAAAGAGCTCATGGCTACTGGTACTTC 598
Qy 304 GGCAAGGCTTGGTCGAGATCTTACCTGGCGTTCAGCTGCTTCTTCACAGTGTGCTCATC 363
Db 599 GGGCAGGTGTGGTGGCGGTGTACCTGGCGCTCGATGTGCTGTTTGCACCTCGTCGATC 658
Qy 364 GTGCACCTGTGGCGCATCAGCTGGACGGTACTGTGTCATCACAGGCGCATCGAGTAC 423
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Qy 424 AACCTGAAGCAGCGCGCGCATCAAGGCCATCATCATCATCATCATCATCATCATCATCAT 482
Db 719 AACCTGAAGCAGCACACACGCGCGTCAAGGCCACCATCATCATCATCATCATCATCAT 778
Qy 483 GCGCGTCACTCTTCTTCCGCGCTCATCTCTCATTCGAGAAAGAGGCGCGCGCGCGCGCC 542
Db 779 GCGCGTCACTCTTCTTCCGCGCTGGTCTCGCTTACCGCCAGCCCGACGCGC----- 831
Qy 543 GCAGCGCGCGCGCGCGCTGGAGATCAACGACCAAGTGGTACGTCTCTCTCGTCGTG 602
Db 832 -----CGCGCTACCGCGAGTGGCGCTCAAGGCCACCATCATCATCATCATCATCAT 886
Qy 603 CATCGCTCTCTTCTTCCGCGCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 662
Db 887 CATCGCTCTCTTCTTCCGCGCTCGCTCATCATCATCATCATCATCATCATCATCATCAT 946
Qy 663 GATGCCAAGCGTGGCGCGCGCGTGGCCAGCCCGCGCGCGGTTCGGACGCGCTCGCGCGC 722
Db 947 AGTGCCCAAGCTGGCGCGCGCTCAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1006
Qy 723 GCGCGC 728
Db 1007 TCGCTC 1012

RESULT 8
GGA2AAR GGA2AAR 855 bp DNA linear GSS 14-SEP-2001
LOCUS GGA2AAR
DEFINITION Chicken alpha2 adrenergic receptor gene fragment probably subtype
a, genomic survey sequence.
ACCESSION AL606540
VERSION AL606540.1 GI:15591915
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE chicken.
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Archosauilia; Aves; Neognathae; Galliformes; Phasianidae;
TITLE Phasianinae; Gallus.
JOURNAL 1 (bases 1 to 855)
REFERENCE 2 (bases 1 to 855)
AUTHORS Hunter, C. and Elgar, G.
TITLE Alpha2 adrenergic receptor gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 855)
AUTHORS Hunter, C.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgm.mrc.ac.uk
Location/Qualifiers
FEATURES
source
1. 855
/organism="Gallus gallus"
/db_xref="taxon:9031"
BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN
Query Match 23.7%; Score 320.2; DB 17; Length 855;
Best Local Similarity 65.8%; Pred. No. 1.6e-48;
Matches 626; Conservative 0; Mismatches 223; Indels 102; Gaps 7;
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Qy 286 ATGGGCTACTGGTACTTCGGCAGAGCTTGGTGCAGATCTACTCGCGCTGCAGCGTGCTC 345
Db 1 ATGGGTTATTGGTACTTCGGCAAGTCTGGTGCAGATCTACTCGGCTTGGACGTGTG 60
Qy 346 TTCTGCACGCTCGTCCATCGTGACCTGTGGCCCATCAGCTGACCGCTACTGGTCCATC 405
Db 61 TTCTGCACCTCTCCATCGTGACATCTGTGGCCCATCAGCTGACCGCTACTGGTCCATC 120
Qy 406 ACACAGGCCATCGAGTACACCTGAAGCGCACCGCCGCGCATCAAGGCCATCATCATC 465
Db 121 ACACAGCCATCGAGTACACCTGAAGCGCACCGCCGCGCATCAAGTGATCATCTTC 180
Qy 466 ACCGTGTGGTCTATCTGGCCGTCATCTCTTCCCGCTCATCTCCATCCAGAGAAG 525
Db 181 ATCGTCTGGTCTATCTCGGCCGTCATCTCTTCCCGCTCATCTCCATAGAGAAG 240
Qy 526 GCGGGGGGGGGCGCGGAGCGCGGAGCCCGCTGCGAGATCAACACACAGAGTGG 585
Db 241 AGTGGGCGAGCGTGGACCAAGTGGGCGGAGGATGCAAGATCAATGACGAGAAGTGG 297
Qy 586 TAGCTCATCTCGTCTGTCATCGGCTCTCTTCTGCTCCCTGCTGCTCATCATGATCTCTGGTC 645
Db 298 TACATCATCTGTCGAGATCGGCTCTCTTCCACCGTGCTCATCATGATCTCTGGTC 357
Qy 646 TAGCTGCGCATCTACAGATCGCAAGCGTGCACCGCGTGCACCCAGCCGCGGGGT 705
Db 358 TAGCTGCGCATCTATCAGATAGCAAGAGCGAAACAGGGTCCGCTGAACAAAG---- 413
Qy 706 CCGAGCGCGTCCGCGCGCGGGGGGACCGAGCGGAGGCGCCCAACCGTCTGGGCCCC 765
Db 414 -----GCCAGAGCGCGGAGAGAAAGAGAAATGGCTTGGCCGAC 453
Qy 766 GAGCGAGCGCGGCGCGGGGGCGAGAGCGGCAACCGCTGCCACCCAGCTCAACGCG 825
Db 454 AAGAGAGACCTG-----CCTGCTCAGCCCCAGCTCAATGGAGAGA 493
Qy 826 GCCCTTGGAGCGCGCGCGCGCGCGCGCACACCGACCGCTGACCTCGAGGAG 885
Db 494 AAGCGCGGAGCTGGGATGGGCGAGG-AGGAGAGGTCAACGGTATAGCATGGAGGA 552
Qy 886 AGTCTGCTTTCCAGCACCGCGCGGCTTCAGGCGCGCGGAGACCCGAGCGCGTCCC 945
Db 553 ACCTCTCTCTTCTGAGCACGAGGAGAACACCC---AGCCCCAAGAAATCAGAGAGACCCCTG 609
Qy 946 CCGGGCAAGGCAAGCGCGAGCGGCGAGGTGCAAGCGCGGCGACAGCTCGCGCGCGC 1005
Db 610 CCGGGAAAGCAAGCAAGTAAGCTGAGCCAGATTAAGCTTGGGACACTTTGGCCAGGAAG 669
Qy 1006 GGGCCGGGGCGACGGGGATCGGGACCGCGCTGCAGGGCGGGGAGGAGCGCTCGGG 1065
Db 670 ACGAGGAGGAGA-----GG 584
Qy 1066 GTTGCAGCGCTGCGCTGCGCGGGCGGCGAGAAACCGGAGAGCGCTTACGTTGCTG 1125
Db 685 AACACCAAGAGGTCCGCGTGGAGGGGCGAGCAGAAACCGGAGAGAAAGTTTCACTTCGTTG 744
Qy 1126 CTGCGCGTGTGTCATCGAGTGTTCGTTGCTGCTGCTGCTTCCCTTCTTCTTCACTACAG 1185
Db 745 CTGCGCGTGTGATGGGGTCTTCGTCATCTGCTGCTGCTTCCCTTCTTCTTCACTACAG 804
Qy 1186 CTCACGGCGCTCGGG-----TGCTCCGTGCCACGACGCTCTTCAAAATTC 1230
Db 805 CTGACCGCGCTGCGAAGAGCTGCTCTGTGCTTCCACCCCTCTTCAAGTTC 855

RESULT 9
BM352981/c 358 bp mRNA linear EST 07-JAN-2002
LOCUS ig69h02.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:A2AA_HUMAN
DEFINITION F08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
ACCESSION BM352981
VERSION BM352981.1 GI:18085339
KEYWORDS EST.
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 358)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ig69h02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 342.
Location/Qualifiers
1..358
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
BASE COUNT 76 a 114 c 115 g 53 t
ORIGIN

Query Match 23.7%; Score 319.4; DB 13; Length 358;
Best Local Similarity 99.7%; Pred. No. 2e-48;
Matches 320; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1026 CCGGACCGCGCTCCAGGGCGGGGAGGAGCGCTCGGGGCTGCCAAGCGCTCGCGCTG 1085
Db 358 CCGGACCGCGCTCCAGCGCCCGGGGAGGAGCGCTCGGGGCTGCCAAGCGCTCGCGCTG 299
Qy 1086 CCGGGGGCGGAGAACCGGAGAGCGCTTCACGTTCTGCTGCGCCGCTCATCGGAGT 1145
Db 298 CCGGGGGCGGAGAACCGGAGAGCGCTTCACGTTCTGCTGCGCCGCTCATCGGAGT 239
Qy 1146 GTTCTGTTGTTGTTGTTTCCCTTCTTCTTCCACCTACACGCTACGCGCGCTCGGGTCTC 1205
Db 238 GTTCTGTTGTTGTTGTTTCCCTTCTTCTTCCACCTACACGCTACGCGCGCTCGGGTCTC 179
Qy 1206 CGTGCCACGACGCTCTTCAAAATTTCTTCTTCTGTTCTGGTCTACTGCAACAGCTCGTTGAA 1265
Db 178 CGTGCCACGACGCTCTTCAAAATTTCTTCTTCTGTTCTGGTCTACTGCAACAGCTCGTTGAA 119
Qy 1266 CCGGCTCATCTACACCATCTTCAACACGAGTTCCCGCGCGGCTTCAAGAGATCCTCTG 1325
Db 118 CCGGCTCATCTACACCATCTTCAACACGAGTTCCCGCGCGGCTTCAAGAGATCCTCTG 59
Qy 1326 TCGGGGGGACAGGAAGCGGAT 1346
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Db 58 TCGGGGGACAGGAGCGGAT 38

RESULT 10
AL530418 867 bp mRNA linear EST 13-FEB-2001
DEFINITION AL530418 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD007E02 5
prime, mRNA sequence.
ACCESSION AL530418
VERSION AL530418.1 GI:12793911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..867
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD007E02"
/lab_host="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH108"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 98 a 315 c 286 g 143 t 25 others
ORIGIN

Query Match 23.5%; Score 317.6; DB 9; Length 867;
Best Local Similarity 76.8%; Pred. No. 4.7e-48;
Matches 407; Conservative 8; Mismatches 102; Indels 13; Gaps 2;

Qy 105 GCTGGTGGCTGGCGGCGCTCATGCTGCTCACCGTGTTCGGCAACGTCGTCTCAT 164
Db 351 GCTGGCTKCCGTTGGGCTTCCCTCATGCTCTTACCCTGTTGGGGCAACGTCGTGGGT 410
Qy 165 CATCGCGCTGTTACAGCGCGCGCTCAAGCGCGCCCAAAACCTTCCTCGTGTCTCT 224
Db 411 GATCGCGCTTCTGACCGCGCGGCGCT - GCGCGCCCAACAAACCTTCCTGCTGTGCT 469
Qy 225 GGCCTGGCGGACATCTCTGTGGCCAGCTCGTATCCCTTTCTCGCTGCCCAACGAGGT 284
Db 470 TGCCTTGGCCGACATCTCTGTGGCCAGCTGCTCATGCCCTTCTCGTTGGCCACGAGCT 529
Qy 285 CATGGCTACTGTTACTTCGGCAAGGCTTGGTGGAGATCTTACTCGCGCTCGACGTGCT 344
Db 530 CATGGCTACTGGTACTTTCGGCGAGGTGKTGGCGGCTGTACTCGCGCTCGATGKTCT 589
Qy 345 CTCTGACAGCTCGTCCATCGTGCACCTGTGGCCCATCAGCTGGACCGCTACTGGTCCAT 404
Db 590 GTTTTGACACTCTGTCATCTGTGTCATCTGTGTCACACAGCTGGACCGCTACTGGKCGT 649
Qy 405 CACACAGGCCATCGAGTACAACTTGAAGCGCACCGCGCGCGCATCAAGGCCATCATCAT 464
Db 650 GACGAGGCGCGTCGAGTACAACTTGAAGCGCACACCAACCGCGCGCTCAAGGCCACCATCGT 709
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Qy 465 CACCGTGGGTCTATCTGGCGGCTCATCTCTCCCGCGCTCATCTCCATTCGAGAGAA 524
Db 710 GCGGTTGGTCAWCTCGGCGGTATCTCTCTCCCGCGCTGCTCTCGCTCTACCGCCA 769
Qy 525 GGGCGGCGCGCGCGCGAGCGCGGAGCGGCGGATCAACGACGAGAGTG 584
Db 770 GCCGACGCGG-----CCGCTACCCGAGTGGGCGCTCAACGACGAGACCCG 817
Qy 585 GTACGTATCTCGTGTGTCATCGGCTCTCTTTCGCTCCCTCGCTCATCA 634
Db 818 GTACATCTCTGCTCTGTCATCGGCTCTCTTTCGCGCCCTGCTCTACA 867

RESULT 11
BO887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
DEFINITION 5', mRNA sequence.
ACCESSION BO887729
VERSION BO887729.1 GI:22279743
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 988)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13739 Row: m column: 06
High quality sequence start: 8
High quality sequence stop: 509.
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Location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone_lib="NIH_MGC_129"
/lab_host="DH108 (phage-resistant)"
/notes="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
is a NIH_MGC Library."
BASE COUNT 158 a 349 c 300 g 181 t
ORIGIN

Query Match 23.5%; Score 317.4; DB 14; Length 988;
Best Local Similarity 74.4%; Pred. No. 5.2e-48;
Matches 432; Conservative 0; Mismatches 136; Indels 13; Gaps 2;

Qy 169 GCGGTGTTACAGCGCGCGCTCAAGCGCGCCCAAAACCTTCTCGTGTCTCTGCCC 228
Db 19 GCTGTGTTGACCGCGAGCAGCTGCGCGCCCGCAGAACCTTCTCTGCTCTCTGCCC 78
Qy 229 TCGCGCG - ACATCTGTGTGGCAGCTCGTATCCCTTCTCGCTGGCCACAGGTCAT 287
Db 79 TCAGCTACACATCTCTGTGGCCACACTGCTGCTCTCTCTGCGCAATGAGCTCAT 138
Qy 288 GGCCTACTGTTACTTCGGCAAGGCTTGGTGGAGATCTTACCTGGCGCTCGACGTGCTCTT 347
Db 139 GGCCTACTGTTACTTCGGGCAAGTGTGTGTGTATACCTGGCACTGGACGTGCTCTT 198
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Qy 348 CTGACGCTGCTCATCTGCACTGCGCCATCAGCTGAGCCGCTACTGTTCCATCAC 407
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Db 199 CTGCACCTCTGCTCCATCTGCACCTGTGTGCGCATTAGTCTGGACCGCTACTGTGCGTGAC 258
|||
Qy 408 ACAGGCCATCGAGTACAACTGAAGCGCAGCGCGCGCCGATCAAGGCCATCATCATCAC 467
|||
Db 259 GCAAGCGGTAGATACAACTGAAGCGCAGCGCGCGCGGTGTCAAGGCCACCATCGTGGC 318
|||
Qy 468 CGTGTGGGTCTCATCTCGGCGCCCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGG 527
|||
Db 319 CGTGTGGGTCTCATCTCGGCTGTCTCTCTTCCCGCTCTCGTCTCTTACCGCGCGCC 378
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Qy 528 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587
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Db 379 CGACGGCGCC-----GCTTATCGCAGTGTGGCGCTCAACGATGAGACCTGGTA 426
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Db 427 CATCTTGTCTCTGATAGGCTCTCTTCTGCGCGCTGCTGCTCTGCTCTGCTCTGCTCTA 486
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Qy 648 CGTGGCGCATCTACGATCGCCAAAGCGTGGCAGCCCGCTGCCACCCAGCGCGCGCGGCTCC 707
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Db 487 TGCGCGCATCTACCGGTGGCCAAAGCTGGCAGCGCTAGCTCAGCGAGAAAGCGCGGCC 546
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Qy 708 GGAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 748
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Db 547 CGCGCGCGCGCGCGCGCGCGCTCCCGACACAGAGAAATGGGC 587
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RESULT 12
BQ302172
LOCUS QV0-BT0263-101299-072-h10 BT0263 Homo sapiens cDNA, mRNA sequence.
DEFINITION QV0-BT0263-101299-072-h10 BT0263 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ302172
VERSION BQ302172.1 GI:20817694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BT0263-
101299-072-h10&t3=1999-12-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 205.
Location/Qualifiers
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/dev_stage="Adult"
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Qy 348 CTGACGCTGCTCATCTGCACTGCGCCATCAGCTGAGCCGCTACTGTTCCATCAC 407
|||
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Qy 408 ACAGGCCATCGAGTACAACTGAAGCGCAGCGCGCGCCGATCAAGGCCATCATCATCAC 467
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Db 259 GCAAGCGGTAGATACAACTGAAGCGCAGCGCGCGCGGTGTCAAGGCCACCATCGTGGC 318
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Qy 468 CGTGTGGGTCTCATCTCGGCGCCCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGG 527
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Db 319 CGTGTGGGTCTCATCTCGGCTGTCTCTTCCCGCTCTCGTCTCTTACCGCGCGCC 378
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Qy 528 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587
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Db 379 CGACGGCGCC-----GCTTATCGCAGTGTGGCGCTCAACGATGAGACCTGGTA 426
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Qy 588 CGTCACTCTGCTGCTGATCGGCTCTCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTA 647
|||
Db 427 CATCTTGTCTCTGATAGGCTCTCTTCTGCGCGCTGCTGCTCTGCTCTGCTCTGCTCTA 486
|||
Qy 648 CGTGGCGCATCTACGATCGCCAAAGCGTGGCAGCCCGCTGCCACCCAGCGCGCGCGGCTCC 707
|||
Db 487 TGCGCGCATCTACCGGTGGCCAAAGCTGGCAGCGCTAGCTCAGCGAGAAAGCGCGGCC 546
|||
Qy 708 GGAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 748
|||
Db 547 CGCGCGCGCGCGCGCGCGCGCTCCCGACACAGAGAAATGGGC 587
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RESULT 13
BQ923710
LOCUS AGENCOURT 8803211 Lupski_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6198830 5', mRNA sequence.
ACCESSION BQ923710
VERSION BQ923710.1 GI:22338741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 15
High quality sequence stop: 535.
Location/Qualifiers
1. .935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6198830"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/lab_host="DH10B"
/lab_stage="adult, 70 yr"
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NotI; Site_2: Sall; cDNA made by oligo-dT priming.
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SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 40 a 109 c 91 g 57 t
ORIGIN

Query Match 20.2%; Score 272.6; DB 14; Length 297;
Best Local Similarity 98.6%; Pred. No. 6.1e-40;
Matches 275; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCCTGACGCGGACCGCGGCAACCGCAGCTGGAAACGGGACCGAGGCGCCGGG 60
Db 11 ATAGGCTCCCTGACGCGGACCGCGGCAACCGCAGCTGGAAACGGGACCGAGGCGCCGGG 70

Qy 61 GCGGCGCGCGCGCGGACCCCTTACTCCCTGCAGTGACGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 71 GCGGCGCTCGGGCACCCCTTACTCCCTGCAGTGACGCTGCTGCTGCTGCTGCTGCTGCTG 130

Qy 121 GGCTGCTCATGCTGCTCAGCGTGTTCGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 131 GGCCTGCTCATGCTGCTCAGCGTGTTCGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 190

Qy 181 AGCGCGCGCTCAAGGCGCGCCCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 191 AGCGCGCGCTCAAGGCGCGCTCCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250

Qy 241 CTGTGGCGCGCTGCTCATCCCTTTCTGCTGGCCAAAC 279

Db 251 CTGTGGCGCGCTGCTCATCCCTTTCTGCTGGCCCTAC 289

RESULT 13
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LOCUS AGENCOURT 8803211 Lupski_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6198830 5', mRNA sequence.
ACCESSION BQ923710
VERSION BQ923710.1 GI:22338741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 935)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 15
High quality sequence stop: 535.
Location/Qualifiers

FEATURES
source

1. .935
/organism="Homo sapiens"
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/lab_host="DH10B"
/lab_stage="adult, 70 yr"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: Sall; cDNA made by oligo-dT priming.

REFERENCE 3 (bases 1 to 966)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
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1..966
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="152E12"
/clone_lib="G"
/note="Genoscope sequence ID : COAG152BC06LP1-end : T7"

BASE COUNT 197 a 283 c 303 g 175 t 8 others

ORIGIN
Query Match 15.9%; Score 214.6; DB 17; Length 966;
Best Local Similarity 75.5%; Pred. No. 2.4e-29;
Matches 265; Conservative 1; Mismatches 85; Indels 0; Gaps 0;
Qy 82 TACTCCTCGAGTGACGCTGAGCTGGTGTGCTGGCGCGCTGCTCATGTGCTCACC 141
Db 608 TACTCCTTAGGGGCYACCGCGGCATCGCGCGCTCGTTAGCTTCTCATCCTGTTACG 667
Qy 142 GTGTTCCGCAACGTGCTCGTTCATCATCGCGCTGTTTACAGAGCGCGCTCAAGCGGCC 201
Db 668 GTGGTCGGGAACATCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 727
Qy 202 CAAACCTCTTCTCTGGTGTCTCTGGCTCGCGCATCTGGTGGCCACGCTCGTCATC 261
Db 728 CAGAACCTCTTCTCTGGTGTCTCTGGCCACCGCGGCATCTGGTGGCCACCTGGTGATG 787
Qy 262 CCTTTCCTCGTGGCCAAACAGGTCTAGGCTACTGGTACTTCGGCAAGGCTTGGTGGAG 321
Db 788 CCCTTCTCCTGGCCAAACGAACCTGATGGGCTACTGGTATTTTCGGCAGAGTCTGGTGGGG 847
Qy 322 ATCTACCTGGCGCTCGACGTGCTCTTCTGCAGTCTGTCCATCGTCACCTGTGCGCCATC 381
Db 848 ATTTATCTGGCTTGGATGTTTATTTCTGCACCTGTGATCGTCCATCTGTGCGCAATA 907
Qy 382 AGCTGGACCGCTACTGGTCCATCACACAGGCCATCGAGTACAACCTGAAG 432
Db 908 AGCTGGACCGCTACTGGTCTGTACGACGCGGTCAGTACAACCTGAAR 958

Search completed: March 11, 2003, 07:39:11
Job time : 23901.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:54:30 ; Search time 1453.85 Seconds
(without alignments) 620.211 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
Sequence: 1 atggggctcctgcagccgga.....ggacacaggaacggaatcata 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 333959956 residues
Total number of hits satisfying chosen parameters: 957848

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database : Published Applications NA:*
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SUMMARIES

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2	444.8	32.9	1344	10 US-09-825-923-1	Sequence 1, Appli
3	443	32.8	1353	9 US-10-077-870-3	Sequence 3, Appli
4	443	32.8	1353	10 US-09-825-923-3	Sequence 3, Appli
5	172.8	12.8	2482	9 US-10-060-795B-10	Sequence 10, Appli
6	170.2	12.6	2625	9 US-09-954-531-995	Sequence 995, Appli
7	168	12.4	1335	9 US-09-349-785-3	Sequence 3, Appli
8	168	12.4	1335	9 US-09-166-334-3	Sequence 3, Appli
9	168	12.4	1335	10 US-09-350-206-3	Sequence 3, Appli
10	168	12.4	2689	9 US-09-349-785-1	Sequence 1, Appli
11	168	12.4	2689	9 US-09-166-334-1	Sequence 1, Appli
12	168	12.4	2689	10 US-09-350-206-1	Sequence 1, Appli
13	151.8	11.2	2140	9 US-10-185-991-1	Sequence 1, Appli
14	147.2	10.9	1645	12 US-10-005-010-1	Sequence 1, Appli
15	147.2	10.9	1973	10 US-08-864-761-3769	Sequence 3769, Appli
16	142	10.5	1185	10 US-09-993-844-13	Sequence 13, Appli
17	142	10.5	3683	10 US-09-895-211-1	Sequence 1, Appli
18	139.8	10.4	694	10 US-09-864-761-17258	Sequence 17258, Appli
19	139.8	10.4	1338	9 US-09-349-785-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:

Query Match 32.9%; Score 444.8; DB 9; Length 1344;
Best Local Similarity 62.4%; Pred. No. 8e-78;
Matches 820; Conservative 0; Mismatches 422; Indels 72;

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QY	138	CACCGTGTTCGGCAACGCTGCTTCGTCATCATCGCCGCTGTTTCAGACGCCGCGCTCAAGGC	197
Db	75	TACCATCTTCGGCAACGCTCTGTGTCTCATCTGCTGCTGTGTGACACGCCGCTCGCTGCGCGC	134
QY	198	GCCCCAAAACCTCTTCTCTGTGTCTCTGCGCTCGCGCGACATCTCTGTGTGGCCAGCTCGT	257
Db	135	CCCTCAGAAACCTGTTCCTGGTGTGCTGGCGCGCGACATCTCTGTGTGGCCACGCTCAT	194
QY	258	CATCCCTTTCTCGCTGGCCAAACAGGTCAATGGGCTACTGTGTTACTTTCGGCAAGGCTTGGTG	317

Db 846 GGGCAGAGAGGGTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAGAGA 905
Qy 934 GAGCGCGTCCCGGGGCAAGGCAAGCGCCGAGCGAGCGAGTGAAGCGGGCAGCAGC 993
Db 906 GGAGGAGGAGGAGGAGAGTGTGAACCCAGGCAAGTGCAGTGTCTCCGGCCTCAGC 965
Qy 994 CTGCGCGGCGCGGGCGCGGGGCGACGGGGATCGGG-----ACGCGGCT 1038
Db 966 TTGAGCGCCCGCTGCAGCAGCCACAGGGCTCCCGGGTGTGGCCACCTACGTGGCCA 1025
Qy 1039 CGAGGCGGGGAGGAGCGCGTGG---GGCTGCCAAGCGCTCGCGCTGGCGCGGGCG 1094
Db 1026 GGTGCTCTGGGAGGGCGGTGGGTGCTATAGTGGGAGTGTGGGCTCGACGGGGCA 1085
Qy 1095 CGAAGACCGCAGAGCGCTTACGTTGCTGCTGCGCGGTGCTACGGAGTGTGTTGGT 1154
Db 1086 GCTGACCGGGAGAGCGCTTACCTTCTGCTGCTGGCTGATGGGCGTTTGTGCT 1145
Qy 1155 GTGCTGTTCCCTTCTTCTTCAATCTTCTGTTGGCTTACTGCAACAGCTCGTTGAA 1265
Db 1146 CTGCTGTTCCCTTCTTCTTCAAGCTACAGCTGGGGCGCATCTGCCGAAGCACTCAA 1205
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Db 1266 CCCTGTTATCTACACCATCTTCAACACAGACTTCCGCGGTGCTTCCGGAGGATCTGTG 1325
Qy 1326 TCG 1328
Db 1326 CCG 1328

RESULT 4

US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyssanen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauphanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein

US-09-825-923-3

Query March 32.8%; Score 443; DB 10; Length 1353;
Best Local Similarity 63.3%; Pred. No. 1.8e-77;
Matches 837; Conservative 0; Mismatches 405; Indels 81; Gaps 7;
Qy 78 CCCTTACTCCCTGTCAGGTGACGCTGCTGGTGTGCTGGCGGCTGCTCATGCTGCT 137
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Qy 138 CACCGTGTTCGGCAACGTCCTGTCATCATCGCGGTGTTACGAGCGCGCGCTCAAGGC 197
Db 75 TACCATCTTCGGCAACGTCCTGGTTCATCTGGCTGTGTGACAGCCGCTCGCTCGCGC 134
Qy 198 GCCCAAAACCTTCTTCTGGTGTCTCTGGCCTCGGCGCACATCTCTGTGGCCACGCTGT 257
Db 135 CCCTCAGAACCTGTTCTTGGTGTGCTGGCGCGCGCGACATCTCTGTGGCCACGCTCAT 194
Qy 258 CATCCCTTCTCGCTGGCCAAAGGTCATGGGCTACTTGGTACTTTCGGCAAGGCTTGGTG 317
Db 195 CATCCCTTCTCGCTGGCCAAAGGTCATGGGCTACTTGGTACTTTCGGCGCACGTTGGTG 254
Qy 318 CGAGATCTACCTGGCGCTCGAGCTGCTCTTGTGACGCTCGTCCATCGTGCACCTGTGGCG 377
Db 255 CGAGGTGTACCTGGCGCTCGAGCTGCTCTTGTGACCTGTCTTGTGACCTGTGGCGC 314
Qy 438 GCGCGCCGCTCAAGGCCATCATCATCGTGTGGTGTCTCTCGCGCTCATCTCTT 497
Db 375 CCGCGCCGCTCAAGTGCATCATCTCTCATCTGTGTGGTGTCTCGCGCGCTCATCTCGCT 434
Qy 498 CCGCGCGCTCATCTCCATCGAAGAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
Db 435 GCGCGCCCTCATCT-----ACAAAGGCGCACAGGCGCGCGCGCGCGCGCGCGCG 485
Qy 558 GCGCTCGAGATCAACGACCAAGAGTGTGTAATCTCTGCTGCTGCTGCTGCTGCTTCTT 617
Db 486 CCAGTGCAGCTCAACAGGAGGCTGTGTACATCTCTGCGCTCCAGCATGGAATCTTCTT 545
Qy 618 CGCTCCCTGCTCATCATGATCTGCTGCTACGTGCGCTATACAGATCGCCAAAGCGTGG 677
Db 546 TGCTCTTGGCTCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCTT 545
Qy 678 CACCGCGTGCACACCA-----GCCCGCGGGGTCCGCGACGCGCTGG 718
Db 606 CAACCGCAGAGTCCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 665
Qy 719 CCGCGCGCGCGCGGG-----CACCAGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCG 760
Db 666 ACCGACCATGTGTGGGGCTTTTGGCTTCAGCAAACTGCCAGCGCGCTGCTGCTGCTTTC 725
Qy 761 GCCCGCAGCGCGCGCGCGCGCG-----GGGCGCAGAGCGCGCGCGCGCGCGCGCGCG 813
Db 726 TGCAGAGAGGTCAACGGAACCTCGAAGTCCACTGGGAGAGAGAGAGAGAGAGAGAGAG 785
Qy 814 CAGCTCAACCG 873
Db 786 TGAAGTACTTGGGACCG 845
Qy 874 GACCTGAGGAGAGCTGCTTTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 933
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Qy 994 CTGCT 1038
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Db 1339 GCCTTCTGAAGATCCTC 1356

RESULT 6

US-09-954-531-995
; Sequence 995, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 995
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-995

Query Match 12.6%; Score 170.2; DB 9; Length 2625;
Best Local Similarity 48.7%; Pred No. 1.3e-24;
Matches 593; Conservative 0; Mismatches 603; Indels 21; Gaps 4;

QY 115 CTGGCGCGCTGCTCATCTGCTCACCCTGTTTCGGCAACGTCGTCTCATCATCGCCGTG 174
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QY 175 TTCAGAGCGCGCTCAAGCGCGCCCAAAACCTTCTCTCTGCTGCTCTCTGCGCTCGGCC 234
Db 343 TCCCGCAGAGCGCGCTCGACACCAACCACTACCTGATCGTCAGCCTCGCAGTGGCC 402
QY 235 GACATCTGTGGCCACGCTCTGTCATCTCTCTCTGCTGGCCAAACAGGTTCATGGCTAC 294
Db 403 GACCTCTCTGTCGCCACACTGTCATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
QY 295 TGGTACTTCGGCAAGGCTTGGTGCAGATCTACCTGGCGCTCGACGCTCTCTTCGACG 354
Db 463 TGGAAATTCAGCAGGATTCACCTGTGACATCTTCTGTCATCTCTGACGCTCATGATGTCACG 522
QY 355 TCGTTCATCTGCTGCTGCGCCATCAGCTGCGCCCTGACCTGCGCCCTGCTCTCATCACAGGCC 414
Db 523 GCGAGCATCTGAACCTTGTGTGCCATCAGCTCGACAGGTACAGCTGTGGCCATGCC 582
QY 415 ATCGAGTCAACCTGAAGCGCAGCGCGCCGCTCATCAAGGCCATCATCATCCGCTGG 474
Db 583 ATGCTGTACAATACGGCTACAGCTCCAGCGCGGGTCACGCTCATGATCTCCATCTC 642
QY 475 GTCATCTCGCGCGTCACT 534
Db 643 TGGGTCTGTCTCTTACCATCT 702
QY 535 GGGGGCG 594
Db 703 AACGAGTGCATCATATGCCAACCGCGCTTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 750
QY 595 TCGTCTGTGATCGGCT 654
Db 751 GTCTCTCTCTACGTCGCT 810
QY 655 ATCTACAGATCGCAAGCGTCGACCCCGCGGTGCGACCCCGCGCGCGCGCGCGCGCGCG 714

RESULT 7

US-09-349-755-3
; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,755
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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QY 775 GCGGCG 834
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QY 835 GAGCG 894
Db 991 GCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACACCGCCACCGAGAGGACCGGTAC 1050
QY 895 TCCGACCAACG 954
Db 1051 AGCCCCATCCACCG 1110
QY 955 GGCAGGCG 1010
Db 1111 CACAGCACTCTCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1170
QY 1011 GGGGCGGAGCGGATCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1070
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QY 1071 CAAGGC--GTGCGCTGCG 1128
Db 1231 AAGACCATGAGCGGTAGAAAGCTCTCCAGCAGAGGAGGAGAAAGCCACTCAGATGCTC 1290
QY 1129 GCGGTGCTCATCGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1187
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QY 1188 --CAGCGCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1245
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QY 1246 TACTGCAAGCTGCTTGAACCGCGTCTATCAGCATCTTCAACACGATTTCCGCGCGC 1305
Db 1411 TATGTCAACAGCGCGGTGAACCCCATCATCTACACACCTTCAACATGAGTTCCGCAAG 1470
QY 1306 GCCTTCAAGAAGATCCT 1322
Db 1471 GCCTTCTGAAGATCCT 1487

QY 600 GTGCATCGGCTCTTCTCGCTCCCTGCTCATATGATCTCTGGTCTACGTGCGCATCTA 659
 Db 606 TTCCACCTCGGAGTTCTTTACGCGCTTCTCTCAGCGTCACTTTTAACTTACGATCTA 665
 QY 660 CCAGATCGCAAGCGTCGACCGGCTGCCACCCAGCCCGGGTCCGGAGCGCGTGGC 719
 Db 666 CTGAACATCCAGAGCGGACCGCTCTCGGCTGATGAGAGGCGAGCGCGGCC 725
 QY 720 CGCGCCCGCGGGGGCACCGAGCGGAGGCGCCCAACGCTCTG---GGCCCCGAGCGCAGCGC 776
 Db 726 CGAGCCCCCTCCGAGGCGCCAGCCCTCACCCACCCCGCTGCTGCTGGGGTGTG 785
 QY 777 GSGCCCGGGGGCGAGCGGCAACCGTGTCCCAACCGAGTCAACGCGGCCCTTGGCGA 836
 Db 786 GCAGAAGGGGCGCGGGAGGCGCATGCGCTGCACAGGTATGGGCTGGGTGAGGCGCGCT 845
 QY 837 GCCCGCGCGCGCGG 852
 Db 846 AGGCGCTGAGGCGCGG 861

RESULT 10

US-09-349-755-1
 ; Sequence 1, Application US/09349755
 ; Patent No. US20020166131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
 ; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/349,755
 FILING DATE: 08-Jul-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,780
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/985,090
 FILING DATE: 04-DEC-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth A. Hanley
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: WNI-032CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2689 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 291..1625
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-349-755-1

Query Match 12.4%; Score 168; DB 9; Length 2689;
 Best Local Similarity 51.4%; Pred. No. 3.5e-24;
 Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGGCTCCCTGCAGCCGACCGGGCAACCGAGCTGGAACCGGACCGGCGCGGGGG 62
 Db 296 GCGCGCGCGCGCGACCGGGCGCTGAAACGTTTCGGGGCGCTGCGCGGCGAGCGCGCG 355
 QY 63 CGGCGCGCGCGCGCACCCCTTACTCCCTGCGAGGTGACGCTACGCTGCTGCTGGCCGG 122
 Db 356 GCGCGCGCGCGCGCGGCTTCTTGGCAGCGCTGACCGCGGCTGCTGGCCGCTCATGGC 415
 QY 123 CTGCTCATGCTGCTACCGTGTTCGGCAACGCTGCTGCTCATCATCGCGGTGTTACGAG 182
 Db 416 GCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
 QY 183 CGGCGCGCTCAAGCG 242
 Db 476 CTGAGCGCTCCG 535
 QY 243 GGTGGCCACGCTGCTCATCCCTTTCTCGCTGGGCAACGAGGTGATGGGTACTGGTACTT 302
 Db 536 CGTCGCGCGCTTCTGCTATCCACTGTATGCTACCTAGCTGCTGACAGGCGCTGGACCTT 595
 QY 303 CGGCAAGGCTTGTGCGAGATCTACCTGCGGCTGCGAGTCTTCTGCACTGCTGCTCAT 362
 Db 596 CGGCGCGCGCTTCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
 QY 363 CGTGCACTGCTGCGCATCAGCGCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
 Db 656 CTTCAACATGCTGCTCATCAGCTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
 QY 423 C---AACCTGAAGCGCACGCGCGCGCATCAAGGCGCATCATCACCTGCTGGGTCTAT 479
 Db 716 CCGGCGCGCGAGCGGTGACACGCGCGCGCGAGTGGCGAAGATGCTGCTGCTGCTGCTGCT 775
 QY 480 CTGCGCGCTCATCTCTTCCGCGCGCTCATCTCCATCGAGAAAGGCGCGCGCGCGCG 539
 Db 776 GGCCTTCTGCTGCTACGAGCGCGCATCTGAGCTGGGAGTACCTGCTCGCGCGCGAGCTC 835
 QY 540 CCGCGAGCGCGCGCGCGCGCGCTGCGAGATCAACGACCAAGAGTGGTACGCTCATCTGCTC 599
 Db 836 CATCCCGAGGCGCACTGTATGCGGAGTTCTTACAACTGGTACTTCTCATCACGCGC 895
 QY 600 GTGCATCGGCTCTTCTGCTCCCTGCTCATCATGATCTCTGCTGCTGCTGCTGCTGCTG 659
 Db 896 TTCCACCTCGGAGTTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTTACGATCTA 955
 QY 660 CCAGATCGCAAGCGTCGACCGCGGTGCGACCCAGCGCGCGCGCGCGCGCGCGCGCGCG 719
 Db 956 CTTGAACATCCAGAGCGCGCACCGCGCTCCGCTGGATGGGCTCGAGAGCGAGCGCGCG 1015
 QY 720 CG 776
 Db 1016 CGAGCGCGCTCCGAGGCGCGCGCTTACACCGCGCGCGCGCGCGCGCGCGCGCGCG 1075
 QY 777 GGGCG 836
 Db 1076 GCAGAAGGGGCGCGCGGAGGCGCATGCGCTGCGACAGGTATGGGCTGGGTGAGGCGCG 1135
 QY 837 GCCCGCGCGCGCGCGG 852
 Db 1136 AGGCGCTGAGGCGCGG 1151

RESULT 11

US-09-166-334-1
 ; Sequence 1, Application US/09166334
 ; Patent No. US20020168708A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
 ; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street

QY 480 CTGGCCGCTCATCTCTTCCGGCGCTCATCTCATCGAAGAGGGCGCGCGCGG 539
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Db 776 GGCCTTCTGCTGTACGACACAGCATCTCTGAGTGGAGTACCTGTCCGGGGCAGCTC 835
QY 540 CCGGAGCGCGCGCGCGCTGCGAGATCAAGACCAAGTGGTACGTCTCATCTCGTC 599
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Db 836 CATCCCGAGGGCCACTGCTATGCCAGTTCCTTCAACTGGTACTTCTCATCAGGC 895
QY 600 GTGATCGGCTCTTCTTGGCTCCCTCCCTCATCATCATCTCTGTTACGTGGCATCTTA 659
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Db 896 TTCACCCCTGAGTTCCTTACGCCCTTCTCAGCGTCACCTTCTTAACCTCAGCATCTA 955
QY 660 CCAGATCCCAAGCGTCCACCCCGCTGCCACCCAGCGCGCGGGTCCGACGCCGCTGC 719
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Db 956 CCGTGAACATCCAGAGGGGCAACCGCTCCGGCTCGAGAGGAGCGAGCGGCC 1015
QY 720 CCGCGCGCGGGGGCAGCGAGCGCGAGCGCGCGCGCTG---GGCCCCGAGCGCAGCGC 776
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

Db 1016 CGAGCCCTCCCGAGGCCAGCCCTCAGCACCACCGCTGCTGGCTGCTGGGCTGCTG 1075
QY 777 GGGCCCGGGGGCGCAGAGCGCGCAACCGCTGCCCAACCGAGCTCAACCGCGCCCTTGGCGA 836
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,334
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,780
; FILING DATE:
; APPLICATION NUMBER: US 08/985,090
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-166-334-1

QY 837 GCCCGCGCGCGCGCGG 852
Db 1136 AGGCGCTGAGCGCGG 1151

RESULT 12
US-09-350-206-1
; Sequence 1, Application US/09350206
; Patent No. US20020099199A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,206
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625

Query Match 12.4%; Score 168; DB 9; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3.5e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;
QY 3 GGGCTCCCTGACGCGGCGGCGACGAGCTGGAACCGGACCGAGGCGCGCGGGG 62
Db 296 GGGCGCGCGCGCGCGCGCTGAACTTCGGGGCGCTGGGGCGAGGCGCGGCG 355
QY 63 CGGCGCGCGCGCGCGCTTACTCCCTGAGGTGAGCGTGTGTCCTGCGCGG 122
Db 356 GCGCGCGCGCGCGCGCTTCTCGGCGCGCTGGAACCGCGGTGCTGGCGGCTCATGGC 415
QY 123 CTGTCTATGCTGCTACCGTGTTCGGCAAGCTGCTGCTCATCATCGCGGTTCACGAG 182
Db 416 GCTGCTATGCTGGCGCGGCTGCTGGCAACCGCTGCTGCTGCTGCTGCGGCGA 475
QY 183 CCGCGCGCTCAAGGCGCGCGCGCGCTTCTCTGCTGCTTCTGCGCTCGCGCGCATCT 242
Db 476 CTCGAGCTCCGCAACCGCAACAACTTCTCTGCTCAACCTCGCGCATCTCCGACTTCT 535
QY 243 GGTGGCCACGCTGCTGCTATCCCTTCTGCTGCGCGCAACGAGGTGCTGCTGCTGCT 302
Db 536 CGTGGCGCGCTTCTGCTATCCCTATGATACCTACGCTGCTGCTGCTGCTGCTGCTG 595
QY 303 CGGCAAGCTTGGTGGAGATCTACCTGCGCTGCGAGCTGCTTCTGCTGCTGCTGCTGCT 362
Db 596 CGCGCGCGCGCTTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
QY 363 CGTGCACCTGTGGCGCATCAGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Db 656 CTTCAACATCGTCTCATCAGCTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
QY 423 C---AACCTGAAGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 716 CCGGGCCACGAGGCTGACACGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775

US-09-350-206-1

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Query Match      12.4%; Score 168; DB 10; Length 2689;
Best Local Similarity 51.4%; Pred. No. 3,5e-24;
Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGCTCCCTGACCGGACCGCGGCAACCGAGCTGGAAACCGGACCGAGCGCGGGGG 62
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QY 63 CGSCGCGCGCGCGCGCGCGCTTACTCCCTGAGGTGAGCTGAGCGGTGCTGGCGCG 122
DB 356 GCGCGCGCGCGCGCGCGCTTCTCGGACGCTGAGCGCGGTGCTGGCGCGCTCATGCG 415

QY 123 CTGTCTATGCTGCTCACCCTGTTCCGCAACGCTCTGCTCATCATCGCGCTGTTCACGAG 182
DB 416 GCTGCTCATGTCGCGCACGCTGCTGGCAACGCGCTGCTGCTGCTGCTGCTGCTGCGCA 475

QY 183 CCGCGCGCTCAAGGCGCGCGCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
DB 476 CTGAGCCTCCGCGCGCGCGCAAAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535

QY 243 GTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
DB 536 GCTGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 595

QY 303 CGGCAAGGCTTGTGCGAGATCTACTGCGGCTCGACGCTGCTTCTGCGCGCTGCTGCTGCT 362
DB 596 CGGCGCGCGCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655

QY 363 CGTGCACTGTGGCGCATGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
DB 656 CTTCAACATCGTGTCTCATGCTGAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715

QY 423 C---AACCTGAAGCGCACCGCGCGCGCATCAAGGCCATCATCACCGTGTGGTGCAT 479
DB 716 CCGGCGCGCGAGGCTGACACCGCGCGCGCATGCGGAGATGCTGCTGCTGCTGCTGCTGCT 775

QY 480 CTGCGCGCTCATCTCTCCCGCGCTCATCTCCCATCGAAGAGAGCGCGCGCGCGCGG 539
DB 776 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835

QY 540 CCGCGAGCGCGCGCGCGCGCGCTGAGATCAACGACGAGAGTGGTACGTCATCTGCTC 599
DB 836 CATCCCGCGAGGCGCATGCTATGCGGAGTCTTCTTACAACTGGTACTTCTCTCATCACGCG 895

QY 600 GTGCATCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
DB 896 TTCCACCTGGAGTCTTTTACCGCTTCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955

QY 660 CCAGATCGCCAAAGCGTGCACCGCGCTGCGACCCAGCGCGCGCGGCTGCGGACCGCGTGC 719
DB 956 CTTGAACATCCAGAGGCGCACCGCTCCGCTCGGCTGATGGGCTCGAGAGCGCGCGCGCC 1015

QY 720 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
DB 1016 CGAGCGCGCTCCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1075

QY 777 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836
DB 1076 GCAGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1135

QY 837 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 852
DB 1136 AGCGCGTGAAGCGCGCG 1151
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RESULT 13

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US-10-185-991-1
; Sequence 1, Application US/10185991
; Publication No. US20030022900A1
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
```

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TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
```

```
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
```

```
ADDRESS: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
```

```
ZIP: 10036
```

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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC
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OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.24
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/185,991
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```
FILING DATE: 28-Jun-2002
```

```
CLASSIFICATION: <Unknown>
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```
PRIOR APPLICATION DATA:
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```
APPLICATION NUMBER: 09/444,783
```

```
FILING DATE: <Unknown>
```

```
ATTORNEY/AGENT INFORMATION:
```

```
NAME: White, John P.
```

```
REGISTRATION NUMBER: 28,678
```

```
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
```

```
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (212) 278-0400
```

```
TELEFAX: (212) 391-0525
```

```
TELEX: <Unknown>
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INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
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LENGTH: 2140 base pairs
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TYPE: nucleic acid
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STRANDEDNESS: single
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TOPOLOGY: unknown
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MOLECULE TYPE: DNA (genomic)
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HYPOTHEetical: N
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ANTI-SENSE: N
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FEATURE:
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NAME/KEY: CDS
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LOCATION: 178..1893
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OTHER INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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US-10-185-991-1
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Query Match 11.2%; Score 151.8; DB 9; Length 2140;

Best Local Similarity 51.9%; Pred. No. 4.7e-21;

Matches 432; Conservative 0; Mismatches 377; Indels 24; Gaps 3;

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QY 18 GGACGCGGCAACGCGAGCTGGAAACCGGACCGAGCGCGCGGGGGCGCGCGCGCCAC 77
DB 387 GGAGCGGGGAGCGCGGGCGCGGCGGACGCTGAATGACGCGCGCGCTCGGGGGACT 446

QY 78 CCCTTACTCTCTCAGGTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 137
DB 447 GGTGGTGAAGCGCGAGCGCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503

QY 138 CACCGTGTTCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
DB 504 GGCGGTGGCAGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563

QY 198 GCCCAAAACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
DB 564 GGTCAACAACTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623

QY 258 CATCCCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
DB 624 ACTGCCCTTCTCGGCCACCATGGAGTCTTGGGCTTCTGGGCTTCTGGGCGCGCTTCTG 683

QY 318 CGAGATCTACCTGGCGCTCGAGTGTCTTCTTGTGACGCTGCTGCTGCTGCTGCTGCTGCTG 377
DB 684 CGAGTATGGCGCGCGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743
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QY 378 CATCAGCTGACCGCTACTGTTCCATCACACAGGCCATCGAGTAAACCTGAAGCGCAC 437
Db 744 CATCTCGTGGACCGTACTGCGGCTGCGCACTACTCAAGTACCCAGCCATCATGAC 803
QY 438 GCGCGCGGCATCAAGGCCATCATCATACCGTGTGGGTCAATCTCGGCGGTCAATCTCTTT 497
Db 804 CGAGCGCAAGCGCGCGCCATCTCTGGCCCTGCTCTGGGTCTAGCCCTGTGTGTCTCGT 863
QY 498 CCGCGCGCTCATCTCCATCGAGAAGAGGGCGGGCGGGCGCCAGCGCGCGAGCC 557
Db 864 AGGCGCCCT-----GCTGGGCTGGAAGAGCGCGGTGCGCCCTCACCAGCG 908
QY 558 GCGCTGCGAGATCAACGACAGAGTGTAGTCTATCTCTGCTGTGATCGGCTCTCTTTCT 617
Db 909 CTTCTGCGGTATACCGAGAGCGGCTAGCTGTCTCTCTCGGTGTCTCTCTCTCTCTCT 968
QY 618 CGCTCCCTCTCATATCATGATCTCTGTCTACGTGCGCATCTACAGATCGC-----CAA 671
Db 969 CTTGCCATGCGGTCTATCTGTGTCTGTACTGCGCGGTGTAGTGTGTCGCGCGAGCAC 1028
QY 672 GCGTGCAGACCGGTGCGACCCAGCGCGGGGTTCGGACCGGTGCGCGCGCGCGCGG 731
Db 1029 CACGCGCAGCCTCGAGGCGCGCTCAAGCGCGAGCGAGGCAAGGCTCTCCAGGTGTGCT 1088
QY 732 GGGCACCGAGCGAGCGCAACGCTCTGGGCGCGAGCGCGCGCGCGCGCGCGCGCG 791
Db 1089 GCGATCTACTGTGCGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCG 1148
QY 792 AGAGCGCAACCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 844
Db 1149 CAAGGCGCACACCTTCCGACGTGCTCTCGGTGCGCGCTGCTCAAGTCTCTCC 1201

RESULT 14
US-10-005-010-1
; Sequence 1, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinschank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; FILE REFERENCE: 36536-BA
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1414)
US-10-005-010-1

Query Match 10.9%; Score 147.2; DB 12; Length 1645;
Best Local Similarity 52.9%; Pred. No. 3.5e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;
QY 67 GCGCGCGCGCACCCCTTACTCTCCCTGCGAGGTGAGCGTGAAGCGGTGCTGCGCGCGCGCG 126
Db 365 GCTTGGATCCAGAGACCTCCAGGGCTCAGATCTCCCTTGGCGTGGTCTTTCGTC 424
QY 127 CTATGCTGCTCACCCTGTTCGGCAACGTGCTGCTGATCATCGCGGTGTTCCAGAGCGCG 186
Db 425 ATCAGACTGGCCACAGTCTCTCCAATGCTTGTACTCACCACCATCTTACTCACCAGG 484
QY 187 GGGCTCAAGGCGCGCGCAACCTCTCTGCTGCTCTGCGCTCGCGCGCGCGCGCGCG 246
Db 485 AAGCTCCACACCCCTGCCAACTACTGATTGGCTCCCTGGCGCACACCGACCTCTTGGT 544

QY 247 GCGAGCTGCTATCCCTTTCTCCTCGGCCAACGAGGTCTATGGCTACTGGTACTTCGGC 306
Db 545 TCCATCTTGGTAATGCCCATCAGCATCGCTTATACCATCACCCACCTGGAACCTTTGGC 604
QY 307 AAGGCTTGGTCGAGATCTACCTGGCGCTCGAGGTCTCTTCTGACGTGCTGCTCATCGTG 366
Db 605 CAAATCTTGTGTGACATCTGGCTGTCTCTGACATCAGTGTGTCACAGCTCCATCTG 664
QY 367 CACCTGTGCGGCATCAGCCTGACCGCTACTGTCTCATCACAGGCCATCGAGTACAAC 426
Db 665 CATCTCTGTCTCTGCTCTGACAGGTACTGGGCAATCAGATGCGCTTGAATACAGT 724
QY 427 CTGAAGCGCAGCGCGCGCATCAAGGCCATCATCATCCGTGTGGTCTATCTCGGCC 486
Db 725 AAACGACGAGCGGTGGCGCACGCGGCCACCATGATGCCATTTGTCTGGGCAATCTCCATC 784
QY 487 GTCATCTCTTCCCGCGCTCATCTCCATCGAAGAGGCGCGCGCGCGCGCGCGCG 546
Db 785 TGCATCTCCATCCCGCGCTCTTCTGGCGGCGAGCGCGCGCGCGCGCGCGCGCG 832
QY 547 CCGCGCGAGCGCGCTGCGAGATCAACGACCGAGGTGTAAGTGTATCTCTGCTGTGATC 606
Db 833 GAGATGTGCGACTGTCTGTGTAACACCTCTCAGATCTCTACACATCTACTCCACCTGT 892
QY 607 GCGTCTCTTCTGCTCTCTGCTCATCATGATCTGCTGTCTAGTGTGCGCATCTACAGATC 666
Db 893 GGGGCTCTTCTACATTTCTCTGCTGTGCTCATCTATATGCGCGGATCTACCGGCT 952
QY 667 GCGAAGCTGCGCACCGCGGTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
Db 953 GCGCGGAACCGCATCTGAATCCACCTCACTCTATGGAAGCGCTTACCACGCGCG 1010

RESULT 15
US-09-864-761-3769/c
; Sequence 3769, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenaheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662

Search completed: March 11, 2003, 23:15:41
Job time : 1465.85 secs

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3769
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049576.15
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
US-09-864-761-3769

Query Match      10.9%; Score 147.2; DB 10; Length 1973;
Best Local Similarity 52.9%; Pred. No. 3.6e-20;
Matches 348; Conservative 0; Mismatches 298; Indels 12; Gaps 1;

Qy 67  GCGCGGCGCACCCCTTACTCCCTGCGAGGTGACGCTGAGCGTGGTGTGCTGGCGGCGCTG 126
Db 1234  GCTTGGGATCCAGGACCCTTCAGGCGCTCAAGATCTCCCTTGGCGTGGTCTTCCGTC 1175

Qy 127  CTCATGTGCTCACCGTGTTCGGCAACGTGCTCGTCTCATCATCGCGGTGTTCAAGAGCGC 186
Db 1174  ATCACACTGGCCACAGTCTCTCCAATGCCCTTGTACTCACCAACATCTTACTACCCAGG 1115

Qy 187  GCGCTCAAGGCGCCCAAACTCTTCTGTGTCTCTGGCTCGGCGGAGATCTCGGTG 246
Db 1114  AAGCTCCACACCCCTGCAACTACTGATGGCTCCCTGGCCACACCGACCTCTTGGTT 1055

Qy 247  GCCAGCTCGTCACTCCCTTCTCGTGGCCAAAGAGTCACTGGGCTACTGTTACTTCGGC 306
Db 1054  TCCATCTTGGTAATGCCCATCAGATCGCTATACCATACCCACACCTGGAACCTTGGC 995

Qy 307  AAGGCTTGTGCGAGATCTACTCGCGCTCGACGTGCTTCTTGACAGTGGTCCATCGTG 366
Db 994  CAAATCTTGTGACATCTGGCTGTCTCTGACATCAGTGTGTCACAGCTCCATCTG 935

Qy 367  CACCTGTGCGCCATCAGCTGGACCGCTACTGGTCCATCACAGGCCATCGAGTACAAC 426
Db 934  CATCTGTGTGCTTGTCTGGACAGGTACTTGGGCAATCACAGATGCCCTTGAATACAGT 875

Qy 427  CTGAAGGCGACGCGCGCGCATCAAGGCCATCATCATCCGTGTGGGTCACTTCGGCC 486
Db 874  AAACGAGGAGCGGTGGCCACGCGGCCACCATGATCGCCATTGTCTGGCCATCTCCATC 815

Qy 487  GTATCTCTTCCGCGCGCTCATCTCCATCGAGAAGAGGCGGCGCGCGCGCGCGCAG 546
Db 814  TGCATCTCCATCCCGCGCTCTTCTGGCGCGAGGCCAAGGC-----CCAGGAG 767

Qy 547  CCGGCCGAGCGCGCTCGGAGATCAACGACAGAGTGGTACGTCACTCTCGTGTGATC 606
Db 766  GAGATGTGGAAGTCTGTGGTGAACACCTCTCAGATCTCTACACCATCTTACTCCACCTGT 707

Qy 607  GGCTCTCTTCTTGGCTCCCTGCCTCATCATGATCTCGTGTCTACGTGGCGCATCTACCAATC 666
Db 706  GGGGCTTCTACATTTCCCTCGGTGTTCTCATCTATATATGGCGGATCTACCGGGCT 647

Qy 667  GCCAAGCGTGCACCGCGGTGCCAGCGCGCGGGTCCGAGCCGCTCGCGCGC 724
Db 646  GCCCGAACCAGCATCTCTGAATCCACCTCTACTATGGGAAGCGCTTTCACACGGGCC 589
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:24:01 ; Search time 1612.04 Seconds
(without alignments)
1885.930 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
Sequence: 1 atgggctccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1350	100.0	1350 23	AAI99917 Human alpha-2AAR e
2	1348.4	99.9	1350 23	AAI99918 Human alpha-2AAR v
3	917	67.9	1733 24	ABQ47500 Oligonucleotide fo
4	917	67.9	1733 24	ABQ47501 Oligonucleotide fo
5	917	67.9	7353 24	ABL32073 Human immune syste
6	917	67.9	7353 24	AAD28363 Human chemically t
7	838	62.1	1733 24	ABQ47498 Oligonucleotide fo
8	838	62.1	1733 24	ABQ47499 Oligonucleotide fo
9	838	62.1	7353 24	ABL32072 Human immune syste

10	838	62.1	7353	24	AAD28362	Human chemically t
11	530.6	39.3	1383	23	AAI99931	Human alpha-2CAR e
12	517.6	38.3	1371	23	AAI99933	Human alpha-2CAR v
13	514	38.1	1382	15	AAQ64890	Human derived adre
14	444.8	32.9	1344	22	AAD04761	Human alpha2B-adre
15	444.4	32.9	1344	22	AAI99906	Human alpha-2AAR t
16	443	32.8	1353	22	AAD04762	Human alpha2B-adre
17	441.4	32.7	1353	23	AAI99905	Human alpha-2AAR t
18	422.2	31.3	2064	12	AAQ14151	Human alpha-2b adr
19	422.2	31.3	2064	18	AAT59499	Human alpha-2b adr
20	328.8	24.4	4850	24	AAD28395	Human chemically t
21	260.6	19.3	1431	18	AAT85635	Balanus amphitrite
22	258.2	19.1	6904	24	ABL32075	Human immune syste
23	258.2	19.1	6904	24	AAD28365	Human chemically t
24	230.2	17.1	4850	24	AAD28394	Human chemically t
25	223.4	16.5	1140	18	AAT88392	Corn barnacle G-pr
26	200.4	14.8	1845	21	AAZ98400	Canine betad-adreno
27	200.4	14.8	1845	21	ABK40732	Dog betad-adrenoce
28	189	14.0	4401	21	AAZ98404	Rhesus monkey beta
29	189	14.0	4401	24	ABK40736	Monkey betad-adren
30	188.6	14.0	1637	22	AAF61182	Human betad-adreno
31	188.6	14.0	1637	22	AAF61183	Human betad-adreno
32	188.6	14.0	1637	22	AAF61184	Human betad-adreno
33	188.6	14.0	1637	22	AAF61185	Human betad-adreno
34	188.6	14.0	1637	22	AAF61186	Human betad-adreno
35	188.6	14.0	1637	22	AAF61187	Human betad-adreno
36	188.6	14.0	1637	22	AAF61188	Human betad-adreno
37	188.6	14.0	1637	22	AAF61189	Human betad-adreno
38	188.6	14.0	1723	21	AAZ38338	Human betad-adreno
39	188.6	14.0	1723	21	AAZ98399	Human betad-adreno
40	188.6	14.0	1723	24	ABK92208	Prostate cancer-as
41	188.6	14.0	1723	24	ABK40731	Human betad-adreno
42	178.2	13.2	1525	21	AAZ98405	Mouse betad-adreno
43	178.2	13.2	1525	24	ABK40737	Mouse betad-adreno
44	177.4	13.1	44242	23	ABL19930	Drosophila melanog
45	177	13.1	1038	23	ABL19931	Drosophila melanog

ALIGNMENTS

RESULT 1
AAI99917
ID AAI99917 standard; DNA; 1350 BP.

XX AC AAI99917;

XX AC AAI99917;

DT 18-FEB-2002 (first entry)

XX Human alpha-2AAR encoding DNA.

DE Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;

XX polymorphic site; allelic variant; cardiovascular disease;

XX central nervous system disease; adenylyl cyclase; MAP kinase activity;

XX phosphorylation; inositol phosphate; alpha-2AAR;

XX GenBank Accession AF281308; chromosome 10; ds.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..1353

XX /*tag= a

XX /product= "alpha-2AAR"

XX WO200179561-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12575.

XX 17-APR-2000; 2000US-0551744.

XX 10-AUG-2000; 2000US-0636259.

XX 19-OCT-2000; 2000US-0692077.

XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX LIGGETT SB, Small KM;
XX
XX WPI; 2001-611728/70.
DR P-PSDB; AAM52122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
FT disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Example 7; Page 151; 163bp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (ggggggggcg) or (B) (ggggggctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (GenBank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;

Query Match	100.0%;	Score 1350;	DB 23;	Length 1350;
Best Local Similarity	100.0%;	Pos. No. 1.4e-203;		
Matches 1350;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ATGGGCTCCTCAGCGGACCGGCGCAACCGAGCTGGAACCGGACCGGCGCGGGG	60		
DB 1	ATGGGCTCCTCAGCGGACCGGCGCAACCGAGCTGGAACCGGACCGGCGCGGGG	60		
QY 61	GGGGGGCGGGCGGACCGGCGGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG	120		
DB 61	GGGGGGCGGGCGGACCGGCGGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG	120		
QY 121	GGGCTCTCATGCTGCTACCGGTGTCGGCAACGCTGCTGCTCATCATCGCGGTTCACG	180		
DB 121	GGGCTCTCATGCTGCTACCGGTGTCGGCAACGCTGCTGCTCATCATCGCGGTTCACG	180		
QY 181	AGCGGCGGCTAAGGCGGCGGCAACCTTCTTCGTTGTTCTTCGCTCGGCGGCGGACATC	240		
DB 181	AGCGGCGGCTAAGGCGGCGGCAACCTTCTTCGTTGTTCTTCGCTCGGCGGCGGACATC	240		
QY 241	CTGGTGGCGGCTCGTCTACCTTCTTCGTTGTTCTTCGTTGTTCTTCGTTGTTCTTCG	300		
DB 241	CTGGTGGCGGCTCGTCTACCTTCTTCGTTGTTCTTCGTTGTTCTTCGTTGTTCTTCG	300		
QY 301	TTGCGCAAGGCTTGGTGGGAGATCTACCTGGGCTCGACGCTGCTTCTTGCACGTCGTC	360		
DB 301	TTGCGCAAGGCTTGGTGGGAGATCTACCTGGGCTCGACGCTGCTTCTTGCACGTCGTC	360		
QY 361	ATCGTGACCTGTGGCGCATCAGCTGGACCGCTACTGCTCCATCACACAGGCCATCGAG	420		
DB 361	ATCGTGACCTGTGGCGCATCAGCTGGACCGCTACTGCTCCATCACACAGGCCATCGAG	420		

QY 421	TACAACTGAAGCGCACGCGCGCATCAAGCCATCATCATCATCATCATCATCATCATCATC	480
DB 421	TACAACTGAAGCGCACGCGCGCATCAAGCCATCATCATCATCATCATCATCATCATCATC	480
QY 481	TCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATTCGAGAAAGGGCGGCGGCGGCGG	540
DB 481	TCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATTCGAGAAAGGGCGGCGGCGGCGG	540
QY 541	CCGAGCG	600
DB 541	CCGAGCG	600
QY 601	TGCATCGGCTCCTTCTTCGCTCCCTCATCATCATCATCATCATCATCATCATCATCAT	660
DB 601	TGCATCGGCTCCTTCTTCGCTCCCTCATCATCATCATCATCATCATCATCATCATCAT	660
QY 661	CAGATCGCCAAAGCGTGCACCCCGCTGCGACCCAGCGCGCGCGCGCGCGCGCGCGCG	720
DB 661	CAGATCGCCAAAGCGTGCACCCCGCTGCGACCCAGCGCGCGCGCGCGCGCGCGCGCG	720
QY 721	GGCG	780
DB 721	GGCG	780
QY 781	CG	840
DB 781	CG	840
QY 841	GGCG	900
DB 841	GGCG	900
QY 901	CAGCG	960
DB 901	CAGCG	960
QY 961	GGCG	1020
DB 961	GGCG	1020
QY 1021	GGATCGGACCG	1080
DB 1021	GGATCGGACCG	1080
QY 1081	CGCTGGCG	1140
DB 1081	CGCTGGCG	1140
QY 1141	GGAGTGTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1200
DB 1141	GGAGTGTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1200
QY 1201	TGCTCGGCG	1260
DB 1201	TGCTCGGCG	1260
QY 1261	TTGAACCGCGCTCATCTACACCATCTTCAACACAGATTCGCGCGCGCGCTTCAAGAAGATC	1320
DB 1261	TTGAACCGCGCTCATCTACACCATCTTCAACACAGATTCGCGCGCGCGCTTCAAGAAGATC	1320
QY 1321	CTCTGTCTGGGGGACAGGAGCGGATCGTG	1350
DB 1321	CTCTGTCTGGGGGACAGGAGCGGATCGTG	1350

RESULT 2
AA199918
ID AA199918 standard; DNA; 1350 BP.
XX
AC AA199918;
XX
DT 18-FEB-2002 (first entry)

XX Human alpha-2AAR variant encoding DNA.
 DE Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; ds.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 1..1353
 FT /*tag= a
 FT /product= "alpha-2AAR"
 FT replace(753,C)
 FT allele /*tag= b
 XX WO200179561-A2.
 XX 25-OCT-2001.
 XX 17-APR-2001; 2001WO-US12575.
 XX 17-APR-2000; 2000US-0551744.
 XX 10-AUG-2000; 2000US-0636259.
 XX 19-OCT-2000; 2000US-0692077.
 XX (LIGG/) LIGGETT S B.
 XX (SMAL/) SMALL K M.
 XX Liggett SB, Small KM;
 XX WPI; 2001-611728/70.
 XX DR P-PSDB; AAM52123.
 XX PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX Disclosure; Page 152; 163pp; English.
 XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (g99gcg99gcg) or (B) (g99gcggtgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idaroxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AAR variant
 CC gene.
 XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
 SX Query Match 99.9%; Score 1348.4; DB 23; Length 1350;
 SX Best Local Similarity 99.9%; Pred. No. 2.6e-203;
 SX Matches 1349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGGCTCCTCCACCGGACCGCGGCAACGCGAGCTGGAACGGGACCGGCGCGGGG 60

1 ATGGGCTCCTCCACCGGACCGCGGCAACGCGAGCTGGAACGGGACCGGCGCGGGG 60
 61 GCGCGCGCGCGCGGACCCCTTACTCCTCGAGGTGACGCTGAGCGTGTGCTGGCC 120
 61 GCGCGCGCGCGGCGACCCCTTACTCCTCGAGGTGACGCTGAGCGTGTGCTGGCC 120
 121 GGCCTGCTCATGCTGCTCAGCGTTCGCGCAACGCTGCTCATCATCGCGGTGTTCAAG 180
 121 GGCCTGCTCATGCTGCTCAGCGTTCGCGCAACGCTGCTCATCATCGCGGTGTTCAAG 180
 181 AGCGCGCGCTCAAGGCGCCCAAAACCTTCTCTGCTGCTCTGCGCTCGCGGACATC 240
 181 AGCGCGCGCTCAAGGCGCCCAAAACCTTCTCTGCTGCTCTGCGCTCGCGGACATC 240
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 241 CTGGTGGCCACGCTGCTCATCCCTTCTCGCTGGCCCAACGAGGTCTACTGGTAC 300
 301 TTGGGCAAGGCTTGGTGGGAGATCTACCTGGCGCTCGACGTGCTTCTTGCACGTGCTCC 360
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 361 ATCTGTGACCTGTGGCCATCAGCTGAGCCGCTACTTGGTCCATCACACAGGCCATCGAG 420
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 421 TACAACTGGAAGCGCAGCGCGCGCCGATCAAGCCATCATCATCAACCGGTGGGTATC 480
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 481 TCGGCGCTCATCTCTTCCCGCGCTCATCTCCATCGAGAAGAGGCGCGCGCGCGCG 540
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Db	573	CACGCCGAA	CGACCTC	CAAAACCC	CGAAACCC	CGAAGCG	GATCC	CGAAACAA	CAAAACAA	514
Qy	961	CGCCGAGCG	AGCCAGG	TGAAGCC	GGGCGAG	CAGCGCT	CCGCGCG	CGCGGG	CGGCGCAGC	1020
Db	513	ACCGAA	CGAAACCA	ATAAAAC	CGAAGCA	CACTAC	CGGACG	CGAACCC	GAAACGACG	454
Qy	1021	GGGATCGGG	ACGCGG	CTGCAGG	CGCGGG	GAGGCGG	TCGGGG	CTGCCA	AGGCGTCG	1080
Db	453	AAAAATC	GAACCG	CGCACT	CAAAAAC	CGAAAAA	AAACCG	CTCGAA	AACTACCAAA	394
Qy	1081	CGCTGGCG	GGCGG	CGAGAA	ACC	CCGAGAA	GCCTT	CAGCTT	CGTCGG	1140
Db	393	CGCTAA	CGCGAA	CGACA	AAACCG	GAAACCG	CTTC	CAGCTT	CGTACT	334
Qy	1141	GGAGTGT	TCGTGTG	CTGGTTC	CCCTTCT	TTCTTCA	CACTAC	ACGCTC	ACGCGCGT	1200
Db	333	GAATA	TATTCG	TAAATAT	ACTAAT	TCCCTTCT	CTTCTT	CACCTAC	ACGCTC	274
Qy	1201	TGCTCCG	TGCGC	AGCGCT	CTTCAA	ATTTCTT	CTTCTGG	TCTGCT	ACTGCA	1260
Db	273	TACTCCG	TAC	CGACGCT	CTTCAA	ATTTCTT	CTTCTA	ATTCG	ACTACTACA	214
Qy	1261	TTGAAC	CCGGT	TCATCT	ACACCAT	CTTTCA	ACACAG	ATTTCC	GCGCGCTT	1320
Db	213	TTAAAC	CCGAT	CATCTAC	ACCATCTT	CAACAC	AGATTT	CCGCGCG	CGCTTCA	1349
Qy	1321	CTCTG	TCGGGGG	ACAGG	AAGCG	ATCGT				
Db	153	CTCTAT	CGAAAAA	CAAAAA	CAAAAA	CAAAAT	CGT			125

RESULT 4

ABQ47501	standard; DNA; 1733 BP.
ID	ABQ47501
XX	AC
XX	ABQ47501;
DT	12-JUL-2002 (first entry)
XX	DE
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
XX	KW
XX	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SNP; cell differentiation; ds.
XX	OS
OS	Homo sapiens.
XX	WO200218632-A2.
PN	XX
XX	07-MAR-2002.
PD	XX
XX	01-SEP-2001; 2001WO-EP10074.
PF	XX
XX	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
XX	(EPIG-) EPIGENOMICS AG.
PA	XX
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
XX	WPI; 2002-371829/40.
DR	XX
XX	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PT	amplicons from chemically treated DNA -
XX	PS
XX	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	PS
XX	This invention describes a novel method for determining the degree of
CC	C methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic

Db 981 GCGCGCGGAAACACCGAACCGAAACCAACGATCTAAACCCCGAACGCAACGCAAC 1040
Qy 781 CCGGGGGCGCAGAGCGCGAAACCGCTGCCACCCAGCTCAACGGCGCCCTCGCGAGCCC 840
Db 1041 CCGAAACCGCAAAACCGAACCGCTACCCACCCAACTCAACGACGCCCTTAACGAAACCC 1100
Qy 841 GCGCGCGCGCGCGCGACCGACCGAGCGCTGAGCTGGAGGAGAGCTGCTTCCGAC 900
Db 1101 GCGCGCGCGCGCGCGCGACCGAGCGCTGAGCTGAGCTGAGGAGAGCTGCTTCCGAC 1160
Qy 901 CACCGCGAGCGCGCTCCAGCGCGCGCGCGAGACCGAGCGCGCTCCCGGGGCAAGCAAG 960
Db 1161 CACCGCGAGCGCGCTCCAGCGCGCGCGCGAGACCGAGCGCGCTCCCGGGGCAAGCAAG 1220
Qy 961 GCCCGAGCGAGCGCTGAGCGCGCGCGCGAGCGCTGCCCGCGCGCGCGCGCGCGAG 1020
Db 1221 ACCCGAGCGAGCGCTGAGCGCGCGCGCGAGCGCTGCCCGCGCGCGCGCGCGAG 1280
Qy 1021 GCGATCGGAGCGCGCTGAGCGCGCGCGCGAGCGCGCTGCCCGCGCGCGCGCGAG 1080
Db 1281 AAAATCGAAACCGCGCTACAAAACCGAAACCGAAACCGCGCTGAAACTACCAAAACGTCG 1340
Qy 1081 CGCTGGCGCGCGCGCGAGAACCGCGAGAACCGCTTCACTGCTGCTGCGCGGTGCTATC 1140
Db 1341 CGCTAACCGCGAACGAAACCGCGAGAAACCGCTTCACTGCTGCTGCTGCTGCTGCT 1400
Qy 1141 GGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1401 GAAATATTCGTAATATATTAATATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1460
Qy 1201 TGCTCGCGCGCGCGCGCGCTGCTTCAAAATTCCTTCTTCTTCTTCTTCTTCTTCTT 1260
Db 1461 TACTTCGCTACCGCGCGCGCTGCTTCAAAATTCCTTCTTCTTCTTCTTCTTCTTCTT 1520
Qy 1261 TTGAACCGCGCTATCTACACCATCTTCAACCACTTTCGCGCGCGCGCTTCAAGAAATC 1320
Db 1521 TTAAACCGCGCTATCTACACCATCTTCAACCACTTTCGCGCGCGCGCTTCAAGAAATC 1580
Qy 1321 CTCTGTCGGGGGACAGAAAGGATCGT 1349
Db 1581 CTCTATCGAAAAACAAAAACGAAATCGT 1609

RESULT 5
ABL32073/c
ID ABL32073 standard; DNA; 7353 BP.
AC ABL32073;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 46.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX

(BFIG-) BPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2002-130909/17.
Nucleic acid comprising fragment of chemically modified gene, useful
for diagnosis and treatment of diseases associated with abnormal
cytosine methylation -
Claim 1; SEQ ID NO 46; 32pp + Sequence Listing; German.
The present invention provides a number of human immune system associated
genes which are modified by the methylation of cytosines. The sequences
can be used in the diagnosis and treatment of immune system disorders,
including eye diseases such as retinopathy, neovascular glaucoma and
macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
rheumatoid arthritis, psoriasis and inflammatory ulcerative bowel
diseases. The present sequence is a gene of the invention.
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
Query Match 67.9%; Score 917; DB 24; Length 7353;
Best Local Similarity 80.0%; Pred. No. 1.2e-135;
Matches 1079; Conservative 0; Mismatches 270; Indels 0; Gaps 0;
Qy 1 ATGGGCTCCCTGACGCGGCGCAACCGAGCTGGAACGGGACCGAGCGCGCGGG 60
Db 2353 ATAAACTCCCTACACCGAACGCGAACAACGGAACGGAACGGAACGCGGAAA 2294
Qy 61 GCGCGCGCGCGCGCGCAACCCCTTACTCCCTGAGGTGAGCTGAGCTGGTGGCTGCC 120
Db 2293 AACGACGCGCGGAAACGCGCGCTTACTCCCTACAAATAACGCTAATATACCTAAC 2234
Qy 121 GCGCTGCTCATCTGCTCAGCGTTCGCGCAACGCTGCTCATCATCGCGCTGTTCAAG 180
Db 2233 GACCTACTCATCTACTCACCCTATTCGCAACGCTGCTGCTCATCATCGCGTATTACG 2174
Qy 181 AGCGCGCGCTCAAGGCGCGCGCAAAACCTTCTGCTGCTGCTGCGCGCGACATC 240
Db 2173 AACCGCGCGCTCAAAACGCGCGCAAAACCTTCTCTAATATCTAACTCGACGACATC 2114
Qy 241 CTGGTGGCGACGCTGCTCATCCCTTTCGCTGGCGCAACGAGGTCATGGCTACTGGTAC 300
Db 2113 CTAATAACCAACGCTGCTCATCCCTTTCGCTAACCAACGAAATCATAACTACTAATAC 2054
Qy 301 TTCGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGCTCTTCTGACAGCTGCTCC 360
Db 2053 TTCGCAAAACCTTATACGAAATCTACCTAACGCTCGAGTACTCTTCTACAGCTGCTCC 1994
Qy 361 ATCGTGCACCTGTGGCGCATCAGCCTTGGACCGCTACTGCTCATCACAGGCCATCGAG 420
Db 1993 ATCGTACACTATAGCCCATCAACCTTAAACCGCTACTAATCTCATCACAAACCATCGAA 1934
Qy 421 TACAACTGAAGCGCGCGCGCGCGCATCAAGCCATCATCATCACCGTGGGTGCTATC 480
Db 1933 TACAACCTAAACGCGCGCGCGCGCATCAAAACCATCATCATCACCGTATAAATCATC 1874
Qy 481 TCAGCGCTCATCTCTTCCGCGCTCATCTCATCGAAGAGGCGCGCGCGCGCG 540
Db 1873 TCGACGCTCATCTCTTCCGCGCTCATCTCATCGAAGAGGCGCGCGCGCGCG 1814
Qy 541 CCGCAGCGCGCGCGCGCGCTGCGAGATCAACGACCAAGTGGTACGCTCATCTCTGCG 600
Db 1813 CCGCAACCGCGCGCGCGCGCTGCGAGATCAACGACCAAGTGGTACGCTCATCTCTGCG 1754
Qy 601 TGCATCGGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 1753 TACATCGACTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1694
Qy 661 CAGATCGCGCAAGGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

Db 1693 CAATCGCCAAACGTCGACCCCGCGTACACCCAAACCGCGAAATCCGAACCGCCGTCGCC 1634
Qy 721 GCCTCCCGGGGGCCGACCGAGCCGCGCCCAACCGTCTGGCGCCCGAGCGAGCGCGGC 780
Db 1633 GCGCCGCCGAAACACCGCAACCGAACCCAGGATCTAAACCCCGAAGCGAACCGGAAC 1574
Qy 781 CCGGGGGGCGAGAGCGGAAACCGTGTGCCACCCAGCTCAACGGCGCCCTTGGCGAGCCC 840
Db 1573 CGAAAAACGCAAAAAACCGAACCGCTTACCGACCCAACTCAACGAGCCCTTAACGAACCC 1514
Qy 841 GCGCCCGCGGGCGCGCGACACCGAGCGCTGGACCTTGGAGAGAGCTCGTCTTCCGAC 900
Db 1513 GCGCCGACCGAACCGCGCGACACCGAGCGCTAAACCTTAAAAAAAACCTGCTTCTCCGAC 1454
Qy 901 CACGCGAGCGGCTCTCAGGGCCCGCGACACCGCGCGTCCCGGGGCAAGGCAAG 960
Db 1453 CACGCGGACGACCTTCAAAAACCCCGCAACCGGACCGGATCCCGGAAACAAAACAAA 1394
Qy 961 GCGCGAGCGAGCGAGTGAAGCGGGGCGACGCTTGCCTGCGCGCGCGCGCGCGGCGGCG 1020
Db 1393 ACCCGAACGAAACCAATAAAACCGAACGAAACCTTACCGCGACGCGAACCGAAAAACGACG 1334
Qy 1021 GGGATCGGACCGCGCTCGAGCGCGGGGAGGAGCGCGTCCGGCTGCGGCTGCCAAGCGCTG 1080
Db 1333 AAATCGAAACCGCGGACTTAAACCGGAAACCGGTCGAAACCTACCAAAACGCTCG 1274
Qy 1081 CGTCCGCGCGGCGGCGAGAACCGCGAGAGCGCTTCAAGTTCGCTGCGCGTGGTGCATC 1140
Db 1273 CGCTAAGCGGACGACAAACCGGAAACCGCTTCAAGTTCGCTGCTAAGCGTAAATCATC 1214
Qy 1141 GAGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1213 GAAATATTGTAATATACTAATATCCCTTCTTCTTCACTACAGCTCACGCTCACGCTCGAA 1154
Qy 1201 TGCTCCGTCGACGACGCTCTTCAAAATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1153 TACTCGTACGACGACGCTCTTCAAAATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1094
Qy 1261 TTGAACCGCGTCACTACACCACTTTCAACCAAGATTTCCGCGCGCTTCAAGAAAGATC 1320
Db 1093 TTAACCCCGATCATCTACACCACTTTCAACCAAGATTTCCGCGCGCTTCAAGAAAGATC 1034
Qy 1321 CTCTCTCGGGGGGACGAGGCGGATCGT 1349
Db 1033 CTCTATCGAAAAACAAAAACGAAATCGT 1005

RESULT 6
AAD28363/c
ID AAD28363 standard; DNA; 7353 BP.
XX
AC AAD28363;
XX
DT 22-APR-2002 (first entry)
XX
DE Human chemically treated genomic DNA #4.
XX
KW Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW drug abuse; migraine; ds.
XX
OS Homo sapiens.
XX
XX
XX WO200202809-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07540.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.

XX
PA (BPIG-) EPIGENOMICS AG.
XX
Pi Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
XX
PS Claim 1; Page 36-40; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviour in schizophrenia
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
SQ Sequence 7353 BP; 1713 A; 384 C; 2140 G; 3116 T; 0 other;
Query Match 67.9%; Score 917; DB 24; Length 7353;
Best Local Similarity 80.0%; Pred. No. 1.2e-135;
Matches 1079; Conservative 0; Mismatches 270; Indels 0; Gaps 0;
Qy 1 ATGGGTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Db 2353 ATAAATCTCTCTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2294
Qy 61 GCGG 120
Db 2293 AAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2234
Qy 121 GCGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 2233 GACCTACTATCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 2174
Qy 181 AGCGCGCGCTCAAGCATC 240
Db 2173 AACCGCGCGCTCAAAACGCATC 2114
Qy 241 CTGGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 2113 CTAAATACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2054
Qy 301 TTGCGCAAGCTTTGGTGGCGAGATCTACCTGGCGCTCGAGCTGCTCTTCTGACAGCTGCTGCT 360
Db 2053 TTGCGCAAACTTAATACGAAATCTACCTAAGCTCGAGTACTCTTCTACAGCTGCTGCTGCT 1994
Qy 361 ATGCTGCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
Db 1993 ATGCTGCACTTATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1934
Qy 421 TACAACCTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480
Db 1933 TACAACCTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1874
Qy 481 TCGGCGCTCATCTCTTCTGCGCGGCTCATCTCCATCGAAGAAAGCGGCGGCGGCGGCGGCGG 540
Db 1873 TCGACCGTCACTCTCTTCTGCGCGGCTCATCTCCATCGAAGAAAGCGGCGGCGGCGGCGG 1814
Qy 541 CCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
Db 1813 CCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1754

QY 601 TGATCGGCTCTTCTTCTGCTCCTGCTCATCATGATCTCTGCTTACGTGGCATCTAC 660
Db 1753 TACATCGACTCTTCTTCTGCTCCTACTCTCATATAATCTTACGTACGATCTAC 1694
QY 661 CAGATCCCAAGGCTGCGACCCGCGTCCACCCAGCGCGCGGGTCCGGACGCGCTCGCC 720
Db 1693 CAAATCGCCAAACGTGCGACCCGCGTACCAACCCACCGCGCGAAATCGGAACGCGCTCGCC 1634
QY 721 GCGCGCGCGGGGCGACCGAGCGCGAGCCCAACCGTCTTGGGCCCCGAGCGAGCGCGGGG 780
Db 1633 GCGCGCGGAAACACCGAGCGCAACCCCAACGATCTAAACCCCGAAGCAACGCGAAG 1574
QY 781 CCGGGGGCGGAGGCGGAGCGGAGCGGCTCCACCCAGCTCAACCGCGCCCTCGCGAGCCC 840
Db 1573 CCGAAAAACGCAAAACCGGACCGCTACCCACCCCACTCAACGACGCGCCCTAACGAACCC 1514
QY 841 GCGCGCGCGCGCGCGACCGAGCGCTGACCTGGAGGAGAGCTCGTCTTCCGAC 900
Db 1513 GCGCGGAGCGGAGCGGAGCGGAGCGGCTAAACCTTAAAAAAAACTCGTCTTCCGAC 1454
QY 901 CACGCCGAGCGGCTCCAGGCGCCCGCAGACCCGAGCGCGGTCCCGGGGCAAGGCAAG 960
Db 1453 CACGCCGAGCGGCTCCAAACCCCGCAACCCGAGCGGATCCCGGAAACAAAAACAAA 1394
QY 961 GCCGAGGAGCGAGGTAAGCGCGGCGACAGCTGCGCGGCGCGGCGCGGGGCGAGC 1020
Db 1393 ACCGGAACGAAACCAATTAACCCGAAACGACCACTACCGGACGCGAACCGAAACGACG 1334
QY 1021 GGGATCGGAGCGCGCTGCGAGGCGCGGGGAGGAGCGGCTCGGGGCTGCAAGGCGTCG 1080
Db 1333 AAATCGAAACCGGACTACAAACCCGAAACAAACCGGTCGAAACTACCAAAACGTCG 1274
QY 1081 CGCTGGCGCGGCGGCGAAGCGGAGAGCGCTTACGTTCTGCTGCGCGGCTGCTCATC 1140
Db 1273 CGTAACCGGAACGACAAACCGCGAAACGCTTACGTTCTGCTGCTGCTGCTGCTGCT 1214
QY 1141 GGAGTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1213 GAAATATTCGTAAT 1154
QY 1201 TGCTCGGCGGACGCGCTCTTCAAAATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1153 TACTCGGTACGACGCGCTCTTCAAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1094
QY 1261 TTGAACCGCGTCACTACACATCTTCAACCAAGATTTCCCGCGGCGCTTCAAGAAATC 1320
Db 1093 TTAAACCGGATCATCTACACATCTTCAACCAAGATTTCCCGCGGCGCTTCAAGAAATC 1034
QY 1321 CTCTGTCGGGGGAGGAGGAGGATCGT 1349
Db 1033 CTCTATCGAAAAAACAACCAACGATCGT 1005

RESULT 7
ID ABQ47498 standard; DNA; 1733 BP.
XX ABQ47498;
XX AC
XX ABQ47498;
DT 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34089.
DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX Homo sapiens.
OS
XX
PN WO200218632-A2.
XX

PD 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EPL0074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1733 BP; 252 A; 211 C; 585 G; 685 T; 0 other;
Query Match 62.1%; Score 838; DB 24; Length 1733;
Best Local Similarity 76.3%; Pred. No. 3.2e-123;
Matches 1030; Conservative 0; Mismatches 320; Indels 0; Gaps 0;
QY 1 ATGGGCTCCCTCAGCGCGGCAACCGAGCTGGAAACGGGACCGAGCGCGGG 60
Db 261 ATGGGTTTTTTGTAGTCGACGCGGGTAACGCGAGTTGGAAACGGGATCGAGCGCTCGGG 320
QY 61 GCGCGCGCGCGGCGCACCCCTTACTCCCTGAGGTGAGCTGACCTGGTGTGCTGCGC 120
Db 321 GCGCGGCTTCGGGTTATTTTTTTTGTAGTGTGAGTGACGTTGACGTTGTTGTTG 380
QY 121 GCGCTGCTATGCTGCTCAGCTGTCGCAACGCTGCTCATCATCGCGTGTTCAG 180
Db 381 GGTTCGTTATGTTTATCGTGTTCGGTAACGTTTCGTTATTCGTTATTCGTTGTTTACG 440
QY 181 AGCGCGCGCTCAAGCGCGCGCCCAAAACCTCTTCTGCTGCTCTCGCTCGCGCCGACATC 240
Db 441 AGTCGCGGCTTTAAGCGGTTTTTAAATTTTTTTTTTGGTGTTCGTTTCGATATT 500
QY 241 CTGGTGCCACGCTCGCTCATCCCTTTCTCGCTGGCCAAACGAGGTCAATGGGCTACTGGTAC 300
Db 501 TTGGTGGTACGTTTCGTTATTTTTTTTTCGTTGTTTAAACGAGTTATGGGTTATTGGTAT 560
QY 301 TTGCGCAAGCGTTGTCGCGAGATCTACCTGGCGCTCGAGCTGCTCTTCGACGCTCGTCC 360
Db 561 TTGCGTAAGGTTTGGTCCGAGATTTATTTGGCGGTTTCGAGCTGTTTTTTTGTACGCTTT 620
QY 361 ATCGTGACCTGTGCGGCATCAGCCTGGAGCGGCTACTGGTCCATCATCACAGGCCATTCGAG 420
Db 621 ATCGGTATTTTGGCGTTATAGTTTGGATCGTTATTGGTTTATTATATAGGTTATCGAG 680

Qy 241 CTGGTGGCCACGCTCGTCATCCCTTTCTCGCTGGCCACGAGTTCATGGGCTACTGGTAC 300
Db 1233 TTGGTGGTTACGTTCTGTTATTTTTTTTCTGGTTAAAGGTTATGGTTATTGGTAT 1174
Qy 301 TTCGGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGAGTGTCTTTCTGACGTCGTCC 360
Db 1173 TTCGGTAAGGTTTGGTGGAGATTTATTTTGGCGTTCGACGTGTTTTTTTGTACGTCGTTT 1114
Qy 361 ATCGTGCACCTGTGCGCCATCAGCCTGGACCGTACTGTGTCATACACAGGCCATCGAG 420
Db 1113 ATCGTGTATTGTGCGGTATTAGTTTGGATCGGTTATTTGGTTTATATATAGGTTATCGAG 1054
Qy 421 TACAACCTGAAGCGCAGCGCGCGCATCAAGGCCATCATCATCCGTGTGGGTCAATC 480
Db 1053 TATTAATTTGAAGGTTAGTCTCGCTGCTATTAAAGTTATTATTATTATTCGTGTGGTTATT 994
Qy 481 TCGGCCCTCATCTCTTTCGCCGCTCATCTCATCGAGAAGGCGCGCGCGCGCG 540
Db 993 TCGGTCGTATTTTTTTTTTCTGCTTATTTTATCGAAGAAGGCGCGCGCGCGGT 934
Qy 541 CCGCAGCGCGCGCGCGCTCGAGATCAACGACACAGAAAGTGTACGTCATCTCGTCG 600
Db 933 TCGTAGTCTGAGTCTCGCTGCGAGATTAAAGATTAGAAAGTGTACGTTATTTCTGTCG 874
Qy 601 TGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCCTGCTACGTGCGCATCTAC 660
Db 873 TGTATCGGTTTTTTTCTGTTTTTGTATTATGATTTTGGTTTACGTGCGTATTTAT 814
Qy 661 CAGATCCCAAGCTCGACCCCGCTGCCACCCAGCCGCGCGGTCGGAGCCGTCGCC 720
Db 813 TAGATCGTTAAGCTGCTATTTCGCTGTTATTTAGTCTGCGGGTTTCGAGCGTCGTCGT 754
Qy 721 CGCGCGCGCGCGCGCGAGCGAGCGCCCAACGCTCTGCGGCCCGAGCCAGCGCGGG 780
Db 753 GCGTCTCGCGGGGTATCGAGCTAGGTTTAAACGTTTGGGTTTCGAGCTAGCGCGGT 694
Qy 781 CCGGGGCGCAGAGCGCGAACCCCTGCCACCCAGCTCAACGCGCGCCCTCGCGAGCCC 840
Db 693 TCGGGGCGTAGAGTTCGAATCGTTGTTATTATTAGTTTAAACGCGTTTTCGCGAGTTC 634
Qy 841 CGCGCGCGCGCGCGCGACCGAGCGCTGACCTGAGAGAGAGCTGCTTCCGAC 900
Db 633 GCGTCTGCGGTCGCGGATATCGACGCTGATTTGGAGGAGATTCGTTTTTCGAT 574
Qy 901 CACGCGAGCGGCTCCAGGCGCCCGCAGACCCGAGCGCGTCCCGGGGCAAGGCAAG 960
Db 573 TACGTCGAGCGGTTTTTAGGTTTTTCGTAGATTCGAGCGCGTTTTCGGGTAAAGTTAAG 514
Qy 961 CCGGAGCGAGCTGAGCGCGGCGACAGCCTGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 513 GTTCGAGCGAGTTAGTGAAGTCGGCGATAGTTTGTGCGCGCGCGGTTCGGGGCGACG 454
Qy 1021 GGGATCGGAGCGCGCTGCGAGGCGCGGGGAGAGAGCGCTGCGGGGTCCCAAGCGCTCG 1080
Db 453 GGGATCGGAGCGCTCGTTGTAGGTTAGGTTGCGGGAGGAGCGCTCGGGGTGTTAAGGCGTCG 394
Qy 1081 CGCTGCGCGGCGCGCAAGCCGCGAGAGCGCTTTCAGTTCTGCTGGCGCTGCTCATC 1140
Db 393 GCTTGGCGCGGCGGTGAATTCGCGAAGCGTTTACGTTCTGTTGGTTCGTGTTATC 334
Qy 1141 GGAGTGTTCGTGCTGCTGCTTCCCTTCTTCTTCACTACACGCTACGCGCGTGGG 1200
Db 333 GGAGTGTTCGTGCTGCTGTTTTTTTTTTTTTTTTTTTTTTTATATACGTTTACGCTGCTGGG 274
Qy 1201 TGCTCGTGCACGCGCTCTTCAAAATCTTCTGTTTCGGTCTACTGCAACAGCTCG 1260
Db 273 TGTTCGTGTTACGTACGTTTTTAAATTTTTTTTTTTTGGTTTCGGTTATTGTAATAGTTTCG 214
Qy 1261 TTGAACCGGCTCATCTACACCACTTCAACACGATTTTCCGCGCGCGCTTCAAGAAGATC 1320
Db 213 TTGAATTCGGTTATTATATATATTTTAAATTTACGATTTTCGTCGGGTTTTTAAAGATTT 154

Qy 1321 CTCCTCGGGGACAGGAAGCGGATCGTG 1350
Db 153 TTTTGTCCGGGGGATAGGAAGCGGATCGTG 124
RESULT 9
ABL32072
ID ABL32072 standard; DNA; 7353 BP.
XX ABL32072;
AC ABL32072;
XX 26-MAR-2002 (first entry)
XX Human immune system associated gene SEQ ID NO: 45.
DE Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antianaemic; cytosine methylation; antiasthmatic;
KW neuropeptide; anti-HIV; anticonvulsant; ophthalmologic;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriasis;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX gene; ds.
XX Homo sapiens.
OS
XX WO200200928-A2.
PN
XX 03-JAN-2002.
PD
XX 02-JUL-2001; 2001WO-EP07537.
PF
XX 30-JUN-2000; 2000DE-1032529.
PR
XX 01-SEP-2000; 2000DE-1043826.
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-130909/17.
DR
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX Claim 1; SEQ ID NO 45; 32pp + Sequence Listing; German.
PS
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
XX Sequence 7353 BP; 1544 A; 384 C; 1956 G; 3469 T; 0 other;
SQ
Query Match 62.1%; Score 838; DB 24; Length 7353;
Best Local Similarity 76.3%; Pred. No. 2.9e-123;
Matches 1030; Conservative 0; Mismatches 320; Indels 0; Gaps 0;
Qy 1 ATGGGTCCTCCAGCCGACCGGGCAACGAGCTGGAACGGGACCGAGCGCGCGGG 60
Db 5001 ATGGGTTTTTTGTAGTCGACCGGGTAACGCGAGTTGGAACGGGATCGAGCGTCGGGG 5060
Qy 61 GCGCGCGCGCGGCCACCCCTTACTCCCTGCAAGTACGCTGACGCTGCTGCTGCGC 120
Db 5061 GCGCGGTTTCGGGTTATTTTTTATTTTGTAGGTGACGTTGCTGCTGCTGCTG 5120
Qy 121 GGCTGCTCATGCTGCTACCGTGTTCGCAACGCTGCTGCTCATCATCCGCGTTCCAG 180
Db 5121 GGTTCGTTATGTTGTTTATTCGTTGTTGTTAAACGTTTCGTTATTTATTCGTCGTTTACG 5180

Qy	181	AGCGCGCGCTCAAAGCGCGCCCAAAACCTCTTCTCGTGTCTCTCGCCCTCGCGCGACATC	240
Db	5181	AGTCGCGGTTTAAGCGGTTTTAAATTTTTTTTTCGGTGTGTTTTCGGTTCGTCGATATT	5240
Qy	241	CTGTTGGCCACGCTCGTCAATCCCTTTCTCGCTGGCCAAAGAGGTCAATGGGTACTGTGTAC	300
Db	5241	TTGTTGGTTACGTTTCGTTATTTTTTTTTTCGTTGGTTAAACGAGTTATGGTTATGGTAT	5300
Qy	301	TTCCGCAAGGCTTGTCGGAGATCTACCTGGCGCTCGACGTCTCTTCGACGTCGTGCC	360
Db	5301	TTCGGTAAGGTTTCGGTCGGAGATTATTTTGGCGTTCGACGTCTTTTTTTGTACGTCGTTT	5360
Qy	361	ATCTGCACTGTGCGGCATCAGCTGGACCGCTACTGCTCCATCACACAGGCCATCGAG	420
Db	5361	ATCGTGTATTGTGCGTTATTAGTTTGGATCGTTATTGGTTTATTATATAGGTTATCGAG	5420
Qy	421	TACAACCTGAAGCGCACGCGCGCGGATCAAGGCCATCATCATCCGTCGTGGGTCACTC	480
Db	5421	TATAATTGAAGCGTACGTCGCTCGTATTAAGAGTTATTATTATTATCTGTGGGTTATT	5480
Qy	481	TCGCGCTGATCTCTTCTCCCGCGCTCACTCCATCGAGAAGAGGGCGCGCGCGGC	540
Db	5481	TCGTCGTATTATTTTTTTTCGTCGTTATTTTATCGAGAAGGGCGCGCGCGCGGT	5540
Qy	541	CCGACGCGGCGAGCGCGCTCGAGATCAACACGACAGAGTGTGTAGTCTCATCTCGTCG	600
Db	5541	TCGTAGTCGTCGAGTCGCGTTCCGAGATTACGATTAGAGTGTGTAGCTTATTTTCGTCG	5600
Qy	601	TGCATCGGCTCTTCTTCGCTCCCTGCCTCATCATGATCTCTGTTCTACGTGCGATCTAC	660
Db	5601	TGTAATCGGTTTTTTTTTCGTTTTTTTGTATTATATGATTTTGGTTTACGTCGTAATTAT	5660
Qy	661	CAGATCCCAAGCGTCGCACCCGCGTCCACCCAGCGCGCGGGTCGGACGCGCTGCC	720
Db	5661	TAGATCGTTAAGCGTCGTATTCGCGTGTATTATTAGTCGTGCGGGTTCCGACGTCGTCTC	5720
Qy	721	GCGCCGCGGGGGGCACCGAGCGACGGCCCAACGCTCTGGGCCCGCGAGCGCAGCGGGC	780
Db	5721	CGTCGTCGCGGGGTATCGAGCGTAGGTTTAACGGTTTGGGTTTCGACGTAGCCGCGGT	5780
Qy	781	CCGGGGGCGCAGAGCGGACCGCTGCCCCACCCAGCTCAACCGCGCCCTTGCGAGCCCC	840
Db	5781	TCGGGGGCGTAGAGTTCGAATCGTTGTTTATTATTAGTTTAAACGGCTTTTGGCGAGTTC	5840
Qy	841	GCGCGCGCGGGCGCGCACACCGACGCTGGACCTGGAGAGAGCTCGTCTTCGAC	900
Db	5841	CGCTCGGTCGGGTCGCGCATATCGACGCGTTGGATTTCGAGGAGAGTTCGTTTTTCGAT	5900
Qy	901	CACGCCAGCGGCTCTCAGGGCCCGCAGACCCGAGCGCGCTCCCGGGCAAGGCAAG	960
Db	5901	TACGTCGAGCGGTTTTTAGGTTTTCGTAGATTCGAGCGCGGTTTCGGGGTAAAGGTAAAG	5960
Qy	961	GCCGAGCGAGCCAGGTGAAGCGGGCGACAGCTGCCGCGCGCGCGCGCGGGGCGACG	1020
Db	5961	GTTTCGAGCGAGTTAGGTGAAGTTCGGGCGATAGTTTGTTCGCGCGCGGTTCGGGGCGACG	6020
Qy	1021	GGGATCGGGACCGCGCTCGACGGCCGGGGAGGACGCTGCGCGCGCGCGCTGCCAAGGCGTCG	1080
Db	6021	GGGATCGGACGTCGCTGTAGGGTCGGGGAGGAGCGCTCGCGGGTGTGTTAAGGCGCTCG	6080
Qy	1081	CGCTGCGCGGGCGGCAGAACCCGAGAGAGCGCTTCAGTTTCGTGCTGGCCGTGGTCACTC	1140
Db	6081	CGTTGCGCGGGCGGTAGAAATCGCGAGAAGCGTTTACGTTCTGTGTGTGGTTCGTTATTC	6140
Qy	1141	GGAGTGTTCGTGTGTGTGGTTCCTTCTTTCACCTACAGCTCAACGCGCTCGGG	1200
Db	6141	GGAGTGTTCGTGTGTGTGGTTTTTTTTTTTTTTTTTTTATTATATACGTTTACGTCGCGG	6200
Qy	1201	TGCTCGTGCACGACGCTCTTCAAAATCTCTCTCTGGTTCGGCTACTGCAACAGCTCG	1260
Db	6201	TGTTTCGTGTACGTACGTTTTTTTAAATTTTTTTTTTTTGGTTCGGTATTCGTAATAGTTCG	6260

Qy	1361	TTGACCCCGGTCATCTACACCATCTTCACACACGATTTCCGCGCGCCTTCAAGAATC	1320
Db	6261	TTGAATTTCGGTTATTTATATATTTTAAATACGATTTTCGTCGCTTTTAAAGAATT	6320
Qy	1321	CTCTGTCGGGGGACAGGAAGCGGATCGTG	1350
Db	6321	TTTGTGCGGGGATAGGAAGCGGATCGTG	6350
RESULT 10			
AAD28362			
ID	AAD28362	standard; DNA; 7353 BP.	
XX			
AC	AAD28362;		
XX			
DT	22-APR-2002	(first entry)	
XX			
DE	Human	chemically treated genomic DNA #3.	
XX			
KW	Human;	cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;	
KW	adrenergic	alpha-1C-receptor; cytosine methylation; therapy; alcoholism;	
KW	behavioural	disorder; neurological; psychiatric; cancer; schizophrenia;	
KW	Tourette's	syndrome; smoking; human immunodeficiency virus dementia;	
KW	drug	abuse; migraine; ds.	
XX			
OS	Homo sapiens.		
XX			
FN	W0200202809-A2.		
XX			
PD	10-JAN-2002.		
XX			
PF	02-JUL-2001; 2001WO-EP07540.		
XX			
PR	30-JUN-2000; 2000DE-1032529.		
PR	01-SEP-2000; 2000DE-1043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
XX			
DR	WPI; 2002-154759/20.		
XX			
PT	Novel	nucleic acid useful for diagnosis and therapy of behavioral	
PT	disorder,	neurological disorder and cancer, comprises a sequence of a	
PT	segment	of chemically pretreated DNA of adrenergic alpha-1C-receptor	
PT	gene	-	
XX			
PS	Claim 1; Page 32-36; 190pp; English.		

The invention relates to nucleic acids comprising a segment of chemically pre-treated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pre-treated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.

positions 961-972 of (iii). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2C, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolfine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2CAR, the sequence includes a 12 nucleotide polymorphic site at nucleotides CC 961-972, absent in the alpha-2CAR variant (AA199933).

XX

SQ Sequence 1383 BP; 164 A; 482 C; 500 G; 237 T; 0 other;

Query Match 39.3%; Score 530.6; DB 23; Length 1383;
Best Local Similarity 65.4%; Pred. No. 5.6e-75;
Matches 876; Conservative 0; Mismatches 419; Indels 44; Gaps 5;

QY 19 GAGCGGGCAACGCGAGCTGGAAACGGGACCGGAGCGCGGGGGCGCGCCCGGGCCACC 78
DB 73 GAGAGGGGCGAGCGGGGGTTGCCAATGCTCGGGGCTTCTGGGGCGCGCGCGCGC 132

QY 79 CTTACTCCCTGCAGGTGACGTGACGCTGGTGTCCTGGCGGGCTCTCATGTGCTC 138
DB 133 CAGTACTCGCGGGCGGTGGCGAGGGCTGGCTGGCGGTGGGGTTCCTCATGCTCTTC 192

QY 139 ACCGTGTTGGCAAGCTGCTCATCATCGCCGCTGTTCAAGCGCGCGCTCAAGCGC 198
DB 193 ACCGTGGTGGCAACGCTGCTGTGTGATGATCGCGCTGTGACACGCGCGCGCTGGCGCG 252

QY 199 CCCAAACCTCTTCTGGTGTCTCTGGCTCGCGCGACATCTGGTGGCCACGCTGTC 258
DB 253 CCACAGAACTCTTCTGGTGTCTGGCTCGCGCGACATCTGGTGGCCACGCTGTC 312

QY 259 ATCCCTTTCTCGCTGGCAACGAGGTGATGGCTACTGGTACTTCCGCAAGCTTGTGC 318
DB 313 ATGCCCTTCTGTTGGCAACGAGCTCATGGCTTACTGGTACTTGGGCAAGTGTGTGC 372

QY 319 GAGATCTACCTGGCGCTCGAGCTGCTCTTCTGCAGCTGCTCATCTGTCACCTGTGCGCC 378
DB 373 GCGGTGTACCTGGCGCTCGATGTGCTGTTTGCACCTGCTCGATCGTATCTGTGTGCC 432

QY 379 ATCAGCTGGACCGCTACTGTGTCATCAACAGGCCATCGAGTACAACTGGAAGCGCAQ 438
DB 433 ATCAGCTGGACCGCTACTGTGTCGTCGTCGTCGAGGCCGTCGAGTACAACTGGAAGCGCA 492

QY 439 CGCGCGCATCAAGCCATCATATCATACCTGTGGTGTGCTGCGCGTCACTCTCTTC 498
DB 493 CCACCGCGCTCAAGCCACCATGCTGCGGTGTGGTGTGCTGCGCGTCACTCTCTTC 552

QY 499 CGCGCGCTCATCTCCATCGAAGAAAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
DB 553 CGCGCGCTGGTCTGCTCTACCGCGACGCCGCGCGG-----CGCGCTACCGCG 600

QY 559 CGCTCGAGATCAACGACCAAGAGTGTGATCTGTCGTGTCATCTGCGTCTCTCTTC 618
DB 601 CAGTGGCGCTCAACGACGAGACCTGGTGTGTCATCTGTCCTGTCATCTGCGTCTCTTC 660

QY 619 GCTCCCTGCTCATCATGATCTCTGCTGTACCTGCGCATCTACAGATGCGCAAGCTGCG 678
DB 661 GCGCGCTGCTCATCATGCTGGCTGTCTACGCGCGCATCTACCGAGTGGCCAAAGCTGCG 720

QY 679 ACCCGCTGCCACCGCGCGCGGGGTTCGGACGCGCGTTCGCGCGCGCGCGCGCGCGCG 738
DB 721 ACGGCAAGCTCAGCGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780

QY 739 GAGCGCAGGCCAAAGGCTCTGGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 798

DB 781 GAAACCGGCTGGCGCGCGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 831

QY 799 GAACCGTGTGCCACCCAGCTAAACGGCGCCCTTGGCGAGC-CCGCGCGCGCGCGCGCGCG 857

DB 832 -----CGCGCGCGCGCGAGCTGGAGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGG 883

QY 858 CGACACGAGCGCGTGAACCTTGGAGGAGAGCTGCTTTCGACACCGCGAGCGCGCTCC 917

DB 884 GCGCGCGCGCGCGCTTTCG 943

QY 918 AGGCGCGCGCGAGACCCGAGCGCGCTCCCGCGGGGCAAGGCAAGCGCGCGAGCGAGCGT 977

DB 944 GCGGTGGAGCGGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGAGTGGGGCGCTGACCGCT 1003

QY 978 GAACCGCGCGAGCAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGGATCGGGAGCGCGCG 1037

DB 1004 CAGGTCTCCCGCGCGCGGCTGCGCGCTCTCTCGCGCGCGAGCTCGCTCGAGTTCT 1063

QY 1038 TGCAAGGCGCGGAGGAGCGCGTCCGGGGCTGCCAAGGCGTCCGCTGGCGCGCGCGCGCA 1097

DB 1064 TCTGTCCGCGCGCGCGCGCGCGCGCGCGAG-----CAGCGTGTGCCCGCGCAAGGTGCGCCA 1118

QY 1098 GAACCGCGAGAGCGGTTTCACTGCTGCGCGCTGCGCGCTCATCGAGTGTTCGTGTGTG 1157

DB 1119 GCGCGCGAGAGCGGCTTCACTTGTGCTGGCTGTGCTCATGCGCGTGTTCGTGTCTCG 1178

QY 1158 CTGCTTCCCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1208

DB 1179 CTGCTTCCCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1238

QY 1209 GCCACGCGAGCTCTTCAAAATCTTCTTCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 1268

DB 1239 GCGCGCGCGCTTCTTCAAGTCTTCTTCTGATCGGCTACTGCAACAGCTGCTCAACCC 1298

QY 1269 GGTCACTTACACCATCTTCAACCAACCATCTTCCGCGCGCTTCAAGAGATCTCTGTGCTG 1328

DB 1299 GGTCACTTACACCGTCTTCAACCAACCATCTTCCGCGCGATCTTCAAGAGATCTCTGCTG 1358

QY 1329 GGGGACAGGAGCGGATC 1347

DB 1359 ACGGAGGAGAGGGGCTTC 1377

RESULT 12
AA199933 standard; DNA; 1371 BP.

XX AA199933;
AC AA199933;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2CAR variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1371
FT /*tag= a
FT /product= "alpha-2CAR"
FT /note= "sequence is deleted for a 12 nucleotide
FT polymorphic site at nucleotides 961-972 of the
FT wildtype sequence (AA199933)"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX

QY 1270 GTCATCTACACCATCTTCAACACGATTTCCGCGCGCTTCAAGAAGATCTCTGTGG 1329
 Db 1293 GTCATCTACACGCTCTTCAACAGGATTTCCGCGGATCTTTAAGACATCTCTTCCGA 1352
 QY 1330 GGGGACAGGAGCGGATC 1347
 Db 1353 CGGAGGAGAGGGGCTTC 1370

RESULT 14
 AAD04761
 ID AAD04761 standard; DNA; 1344 BP.
 XX
 AC AAD04761;
 DT 04-JUL-2001 (first entry)
 DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
 XX
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..1344
 FT /*tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 FT variant protein"
 XX
 PN W0200129082-A1.
 XX
 XX 26-APR-2001.
 XX
 XX 20-OCT-2000; 2000WO-FI00913.
 XX
 XX 22-OCT-1999; 99US-0422985.
 XX
 XX (JUVA-) JUVANTIA PHARMA LTD OY.
 XX
 XX Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssönen K;
 PI Salonen R, Kauhainen J, Valkonen V;
 XX
 XX WPI; 2001-300318/31.
 DR P-PSDB; AAE00989.
 XX
 XX New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 XX Claim 3; Page 24-26; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
 CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
 CC 18 amino acids (amino acids 294-311), located in the third intracellular
 CC loop of the receptor polypeptide. The variant is obtained by deletion of
 CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
 CC gene is located on chromosome 2. Alpha2-AR mediate many of the
 CC physiological effects of the catecholamines, norepinephrine and
 CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
 CC a mammal suffering from vascular contraction of coronary arteries and a
 CC disease involving vascular contraction of coronary arteries which is
 CC clinically expressed as coronary heart disease (CHD), unstable chronic
 CC angina pectoris which is clinically expressed as Prinzmetal's variant
 CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
 CC gene therapy.
 XX

SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
 Query Match 32.9%; Score 444.8; DB 22; Length 1344;
 Best Local Similarity 62.4%; Pred. No. 1.7e-61;
 Matches 820; Conservative 0; Mismatches 422; Indels 72; Gaps 5;
 QY 78 CCCTTATCTCCCTGCAGGTGACGCTGACGCTGTGGTGTGGCTGGCGGCTGCTCATGTGCT 137
 Db 15 CCCTTATCTCCCTGCAGGCCACAGCGGCATAGCGGGCGCATCACCTTCTCTCTTCTT 74
 QY 138 CACCGTGTTCGGCAACGTGCTGTCATCATCGCGTGTTCACGAGCGCGCGCTCAAGGC 197
 Db 75 TACCATCTTGGCAACGCTCTGGTTCATCTGGTGTGTGTTGACAGCGCTCGTGGCGC 134
 QY 198 GCCCAAAACCTCTTCTGTGTGTCTCTGGCTCGGCGACATCTCGTGGCCACGCTGCT 257
 Db 135 CCTCAGAACCTGTTCTGTGTGTGCTGGCGCGCGACATCTGTGTGGCCACGCTCAT 194
 QY 258 CATCCCTTCTCGTGGCCCAACGAGGTGTCATGGGTACTGTGTTACTTCGGCAAGCTTGGTG 317
 Db 195 CATCCCTTCTCGTGGCCCAACGAGGTGTCATGGGTACTGTGTTACTTCGGCGCGACGTTGGTG 254
 QY 318 CGAGATCTACCTGCGGCTCGACGCTCTTCTGCACTGCTGTCATCTGTCACCTGTCGCGC 377
 Db 255 CGAGGTGTACCTGCGGCTCGACGCTCTTCTGCACCTGTCATCTGTCACCTGTCGCGC 314
 QY 378 CATAGCCTGACCGCTACTGTTCCATCACACAGGCCATCGAGTACAACTGAAAGCGCAC 437
 Db 315 CATAGCCTGACCGCTACTGTTCCATCACACAGGCCATCGAGTACAACTGAAAGCGCAC 374
 QY 438 GCGCGCGCATCAAGGCCATCATCATCACCGTGTGGTTCATCTCGGCGCTCATCTCTT 497
 Db 375 CCGCGCGCATCAAGTGCATCATCTCTGTTGTGCTCATCGCGCGCTCATCTCTCT 434
 QY 498 CCGCGCGCTCATCTCCATCGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
 Db 435 GCGCGCGCTCATCT-----ACAGGGCGACAGGGCGCGCGCGCGCGCGCGCGCGCGCG 485
 QY 558 GCGCTGCGAGATCAACGACAGAGTGTGTCATCTGTCGTGTCATCTGCGCTCTCTTCTT 617
 Db 486 CCAAGTCAAGCTCAACAGGAGGCTGTTGATCATCTGCGCTTCCAGCATCGGATCTTCTT 545
 QY 618 CGCTCCCTGCTCATCATGATCTGTTGTCATGTCGTCATCTACAGATCGCAAGCGTCG 677
 Db 546 TGCTCTTCTGCTCATCATGATCTTGTCTACTGCGCATCTACTGTCGTCATCTGTCGTC 605
 QY 678 CACCGCGCTGCCACCA-----GCGCGCGGCTCGGCGCGCGCGCGCGCGCGCGCGCG 718
 Db 606 CAACCGCAGAGTCCAGGGCGCAAGGGGGGCGCTGGGCGAGGTGAGTCCAGCAGCGCGCG 665
 QY 719 CCGCGCGCGCGGGGCGCACCGAGCGCGAGGCCAACCGTCTGGGCG----- 763
 Db 666 ACCGACCATGTTGGGCTTTGGCTCAGCCAACTGCGAGCGCTGCGCTCTGTGGTTC 725
 QY 764 -----CCGAGCGCAGCG 812
 Db 726 TGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGGAGAGGAGGAGGAGGAGACCC 785
 QY 813 CCAGCTCAACGCGCGCTTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 872
 Db 786 TGAAGTACTGGGACCGCGGCTTGGCCACCGAGTTGGCTGCCCTTCCCACTCAGGCCA 845
 QY 873 GGACCTGGAGGAGTCTGCTTTCGACCAACCGCGAGCGGCTTCAGGGCGCGCGCGAGACC 932
 Db 846 GGGCAGAGAGGAGTGTGTTGGGGCATCTCCAGAGGATGAAGCTGAAGAGGAGGAGAGA 905
 QY 933 CGAGCGCGTCCCGGGGCAAGGCAAGCGCGCGAGCGCGAGGTGAAGCGGGCGAG 992
 Db 906 GGAGGAGGAGGAGTGTGAACCCAGCGAGTGCATGTCTCGGCTCAGCTTGCAGGCC 965
 QY 993 CTTGCG 1052
 Db 966 CCGCTGCGCAGCAGCG 1025

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Db 606 CAACCCGACAGGTCCACGGGCCAAAGGG--GGGGCTTGGCAGGGTGAGTCCAAGCAGGCC 663
Qy 738 CGAGCGCAGGCCCAACGGTCTGGGGCCCGAGCGCAGCGGGCCCGGGG-----GGCGCA 792
Db 664 CGACCCGACCATGGTGGGGCTTTGGGCTCAGCCAACTGCCAGCCCTGSCCTCTGTGGCT 723
Qy 793 GAGGCCGAAACCGCTGCCCCACCCAGCTCAACGGCGCCCCCTGGCGAGCCCGCGGCCGGG 852
Db 724 TCTGCCAGAGGTTCAACGGACACTCGAAGTCCACTGGGAGAGGAGGGGAGACC 783
Qy 853 CCGCGGACACCGACCGGCTGGACCTGGAGGAGAGTCTCTCCAGCACCGCCGAGCGG 912
Db 784 CCTGAAGATACTGGGACCCGGGCTTGCACCCAGTTGGGCTGCCCCCTCCCAACTCAGGC 843
Qy 913 C-----CTCAGGGCCCCGACAGCCCGAGCGCG 940
Db 844 CAGGGCCAGAGAGGGTGTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGGAGAG 903
Qy 941 GTCCCCGGGGCAAGGCAAGGCCCGAGCGCAGGTGAAGCCGGCGCAGAGCCTGCCGC 1000
Db 904 GAGGAGGAGGAGTGTGAACCCAGGCAAGTCCAGGTCTCCGGCCTCAGCTTGACGC 963
Qy 1001 GGGCGGGCGGGGGGACCGGGATCGGG-----ACGCGGCTGCAGGGC 1045
Db 964 CCCCCGCTGCAGCAGCCACAGGGCTCCGGGTGCTGGCCACCCCTACGTGGCCAGGTGCTC 1023
Qy 1046 CGGGGAGGAGCGGCTCGG---GGCTGCCAAGCGCTCGCGCTGGCGCGGGCGGCAGAAC 1101
Db 1024 CTGGGCAGGGCGGTGGTGTATAGGTGGCAGTGTGGCGTGAAGGGCGCAGCTGACC 1083
Qy 1102 CGCGAGAAAGCGCTTCAGCTTCGTCTGCTGGCCGTGATCGAGTGTTCGTGGTGTCTGG 1161
Db 1084 CGGAGAAAGCGCTTCACCTTCGTCTGCTGTGTGTCAATTGGCGTTTTTGTGTCTGTCTGG 1143
Qy 1162 TTCCCTTCTTCTTCACCTACAGCTCAGCGCTCAGCGCGTGG-----GTGCTCCGTGCCA 1212
Db 1144 TTCCCTTCTTCTTCAGCTACAGCTGGGGGCCATCTGCCCGAAGCACTCAAGGTGCC 1203
Qy 1213 CGCAGCTCTCAATCTTCTTCTGCTGGCTACTGCAACAGCTCGTTGAACCCGGTC 1272
Db 1204 CATGGCTTCTCCAGTCTTCTTCTGGATCGGCTACTGCAACAGCTCACTGAACCTGTT 1263
Qy 1273 ATCTACACCATCTTCAACACGATTTCCGGCGCCCTTCAAGAGATCTCTGTG 1328
Db 1264 ATCTACACCATCTTCAACACGACTTCCGGCGTCCCTTCCGGAGATCTCTGTGCCG 1319

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Job time : 1646.04 secs

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:31:11 ; Search time 95.1114 Seconds
(without alignments)
4352.932 Million cell updates/sec

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Perfect score: 1350
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Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	12.9	3335	1 US-07-676-174A-1	Sequence 1, Appli
2	168	12.4	1335	2 US-08-985-090-3	Sequence 3, Appli
3	168	12.4	1335	3 US-09-165-543-3	Sequence 3, Appli
4	168	12.4	2689	2 US-08-985-090-1	Sequence 1, Appli
5	168	12.4	2689	3 US-09-165-543-1	Sequence 1, Appli
6	166.4	12.3	1335	3 US-09-167-354-6	Sequence 6, Appli
7	166.4	12.3	1335	4 US-09-642-855-6	Sequence 6, Appli
8	166.4	12.3	1335	4 US-09-642-514-6	Sequence 6, Appli
9	166.4	12.3	2699	3 US-09-167-354-5	Sequence 5, Appli
10	166.4	12.3	2699	4 US-09-642-855-5	Sequence 5, Appli
11	166.4	12.3	2699	4 US-09-642-514-5	Sequence 5, Appli
12	153	11.3	2428	3 US-08-475-742-15	Sequence 15, Appli
13	151.8	11.2	2140	1 US-08-334-698-1	Sequence 1, Appli
14	151.8	11.2	2140	1 US-08-228-932-1	Sequence 1, Appli
15	151.8	11.2	2140	1 US-08-468-939-1	Sequence 1, Appli
16	151.8	11.2	2140	2 US-08-406-855A-1	Sequence 1, Appli
17	151.8	11.2	2140	2 US-08-722-190-1	Sequence 1, Appli
18	151.8	11.2	2140	3 US-08-244-354-1	Sequence 1, Appli
19	151.8	11.2	2140	3 US-09-206-899-1	Sequence 1, Appli
20	151.8	11.2	2140	4 US-09-444-783-1	Sequence 1, Appli
21	151.8	11.2	2140	4 US-09-688-415-1	Sequence 1, Appli
22	151.8	11.2	2140	5 PCT-US95-04203-1	Sequence 1, Appli
23	151	11.2	3335	1 US-08-194-338-1	Sequence 1, Appli
24	150.6	11.2	1621	1 US-08-722-001-13	Sequence 13, Appli
25	150.4	11.1	1956	1 US-08-313-553-6	Sequence 6, Appli
26	150.4	11.1	1956	3 US-08-767-993-6	Sequence 6, Appli
27	150.2	11.1	1776	1 US-08-722-001-29	Sequence 29, Appli

28	147.2	10.9	1645	2 US-08-461-812-1	Sequence 1, Appli
29	142	10.5	1134	1 US-08-087-772A-14	Sequence 14, Appli
30	142	10.5	1227	1 US-07-916-901-1	Sequence 1, Appli
31	142	10.5	3683	4 US-08-450-962-1	Sequence 1, Appli
32	141	10.4	1610	1 US-08-056-051-5	Sequence 5, Appli
33	141	10.4	1610	1 US-07-928-611-21	Sequence 21, Appli
34	141	10.4	1610	2 US-08-487-811A-21	Sequence 21, Appli
35	141	10.4	1610	4 US-09-060-694-21	Sequence 21, Appli
36	141	10.4	1610	4 US-09-378-074-21	Sequence 21, Appli
37	141	10.4	1610	5 PCT-US93-07370-21	Sequence 21, Appli
38	140.8	10.4	1581	1 US-08-313-553-8	Sequence 8, Appli
39	140.8	10.4	1581	3 US-08-767-993-8	Sequence 8, Appli
40	140.4	10.4	1227	1 US-08-351-473B-7	Sequence 7, Appli
41	139.8	10.4	1338	3 US-09-165-543-6	Sequence 6, Appli
42	139.8	10.4	1690	2 US-08-461-812-3	Sequence 3, Appli
43	139.8	10.4	3244	3 US-09-165-543-4	Sequence 4, Appli
44	138.2	10.2	1601	1 US-08-722-001-7	Sequence 7, Appli
45	138.2	10.2	1997	1 US-08-722-001-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Vantor, J. Craig
; TITLE OF INVENTION: Octopamine receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,174A
; FILING DATE: 19910328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-8944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2121
; US-07-676-174A-1

Query Match 12.9%; Score 174; DB 1; Length 3335;
Best Local Similarity 56.2%; Pred. No. 2.8e-23;
Matches 352; Conservative 0; Mismatches 265; Indels 9; Gaps 1;
Oy 128 TCATCGTCTCACCAGTGTCCGCAACGTCGTGTCATCATCGCGTGTTCACGAGCGCG 187
Db 674 TTATCGTCTGACCATCATCGGGAACATCCTGTTGATTCTTGAGTGTCTTCACTACAAGC 733

188 CGCTCAAGGCGCCCAAAACCTCTTCTGGTGTCTCTGGCTCGGCGGACATCCTGGTGG 247
Db |||||
734 CGCTGGCGATCGTCAGAACTTCTTATAGTTTCGCTGGCGGTGGCGATCTCACGGTGG 793
Qy 248 CCACGCTCGTCATCCCTTCTCGCTGGCCCAACAGAGTTCATGGGTACTGTACTTCGGCA 307
Db |||||
794 CCCTTCGTGCTGCTCCCTTCAACGTGGCTTACTGATCCTGGGGCGCTGGAGTTGGCA 853
Qy 308 AGGCTTGGTGGAGATCTACCTGGGGTTCAGCGTGTCTTCTGCACTGTCATCGTGC 367
Db |||||
854 TCCACCTGTGAAGCTGTGGCTACCTGCGACGTGTGTGCTGCACTAGCTCCATCTCTGA 913
Qy 368 ACCTGTGGCCATCAGCTGAGCGCTACTGGTTCATCACAGGGCCATCGAGTCAAC 427
Db 914 ACCTGTGTGCATAGCCCTCGACCGTACTGGGCCATTACGGACCCCATCAATATGCC 973
Qy 428 TGAAGCGCACCCCGCGGCATCAAGGCCATCATCATCACCGTGTGGGTCTATCTCGGCCG 487
Db |||||
974 AGAAGAGACCGTTGGTGGCTCTGCTCTCTCATCTCGGGGTGTGGCTACTTTGCTGC 1033
Qy 488 TCATCTCTTCCCGCGCTCATCTTCATTCGAGAAAGAGGGCGGGCGGCCCGCAGC 547
Db 1034 TGATAAGTAGTCCGCGCTTGTATCGC-----TGGAAACGATGGCGCGAGGTTCA 1084
Qy 548 CGGCGGAGCGCGCTGGAGATCAACGACAGAGTGTGTAGCTCATCTCGTGTGCATCG 607
Db 1085 CAAGCGGACCCCTGCGAGTGCACCTCGCAGCGAGGCTACGTGATCTACTCTCGCTGG 1144
Qy 608 GCTCTTCTTTCGCTCCCTGCTCATCATGATCTCTGCTTACGTGCGCATCTACGATCG 667
Db 1145 GCTCTTCTTATTCGCTGGCCATCATGAGTCTGCTACATCGAGTCTTCTGGCCA 1204
Qy 668 CCAAGCTGCGACCGCGTGCACCCAGCGCCCGGGGTCCGAGCGCGTCCGCGCGCGC 727
Db 1205 CGCGCGCGCGCTTAAGGAGCGAGCCAGGGCCAAACAAGCTTAAACAGATCGCTCTGA 1264
Qy 728 CGGGGGCACCGAGCGAGGCCCAAC 753
Db 1265 CCACTGAGCTCGAGCCGATGGCAAC 1290

RESULT 2

US-08-985-090-3

; Sequence 3, Application US/08985090

; Patent No. 5885893

; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl

; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/985,090

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jean M. Silveri

; REGISTRATION NUMBER: 39,030

; REFERENCE/DOCKET NUMBER: MNI-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-08-985-090-3

Query Match 12.4%; Score 168; DB 2; Length 1335;

Best Local Similarity 51.4%; Pred. No. 3e-22;

Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

Qy 3 GGGCTCCCTGAGCGGACGGGGCAACGGAGCTGGAAACGGGACCGAGGCGCGGGGG 62
Db 6 GGGCGGCGCCCGGACGGGCGCTGAACGCTTCGGGGGCGCTGGCGGCGAGCGCGGC 65
Qy 63 CGGCGCCCGGGCCACCCCTTACTCCCTGCAAGGTGACGCTGAGCTGTGTGCTGGCGG 122
Db 66 GCGGGCGGGGCGCGCGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCGCGCTCATGGC 125
Qy 123 CCGTCTCATGCTGCTCACCCTGTTGGCAACGCTGCTGTCATCATCGCCGTTTCACGAG 182
Db 126 GCTGCTCATGTTGGGCAACGGGTGCTGGGCAACGCGTGTGTCATGCTCGCTTCGTGGCGA 185
Qy 183 CGCGCGCTCAAGGCGCCCAAACTCTTCTGTGTGTCTCTGGCCTCGGCGGCATCCT 242
Db 186 CTCGAGCCTCGCACCCAGAACACTTCTTCTGCTCAACCTCGCCATCTCCGACTTCT 245
Qy 243 GGTGCGACGCTGCTATCCCTTCTCGCTGGCCAAACGAGTGTATGGGCTACTGGTACT 302
Db 246 CGTCGGCGCTTCTGATCCCACTGTATGTATACCTCATGTCGTGTCAGCGCGCTGGACCT 305
Qy 303 CGGCAAGCTTGGTGGAGATCTACCTGGCGCTCGAGTGTCTTCTGACGTCGTCCAT 362
Db 306 CGGCGGGGCTCTGCAAGCTGTGGTGTAGTGAGTACCTGCTGTGACCTCTCTGTC 365
Qy 363 CGTGACCTGTGCGCCATCAGCCTGGACCGTACTGTGTCATCACAGGCCATCGAGTA 422
Db 366 CTTCAACATCGTGTCTATCAGTACGACCGCTTCTGTGCGGTACCCGAGCGGTCTATA 425
Qy 423 C---AACCTGAAGCCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGGTTCAT 479
Db 426 CGGGCCCGCAGCAGGCTGACACGCGCGGGCAGTGGGAAGATGCTGTGGTGTGGTGTCT 485
Qy 480 CTCGGCGCTATCTCTTCCGCGCTCATCTCCATCGAGAAGAGGGCGCGCGCGG 539
Db 486 GGCCTTCTGTGTACGACAGCCATCTGAGTGGAGTACCTGTCCGGGGGAGCTC 545
Qy 540 CCGGACGCGCGCGGAGCGCGCTGCGAGATCAACGACAGAAAGTGTACGTCTCTGTC 599
Db 546 CATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTACAACTGGTACTTCTCATCACGCG 605
Qy 600 GTGCAATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCTTGTGTCTACGTGCGGCTTA 659
Db 606 TTCCACCTCTGGAGTTCTTTAGCGCTTCTCAGCGTCACTTCTTAACTCTCAGCATCTA 665
Qy 660 CCAGATCGCAAGCTGCGACCGCGGTGCCACCGCGCGGGTCCGAGCGCGCTCGC 719
Db 666 CTTGAACATCCAGAGGCGACCCGCTCGGCTGATGGGCTCGAGAGGAGCGCGGCGC 725
Qy 720 CGCGCGCGCGGGGCGACCGAGCGGAGGCCCAACGGTCTG---GGCCCCGAGCGAGCGC 776
Db 726 CGAGCCCCCTCCCGAGGGCCAGCCCTCACACCCCGCTGCTGCTGGGCTGCTG 785
Qy 777 GGGCGCGGGGCGGAGAGCGGAGAACCGCTGCCCAACCGAGTCAACGCGCCCTTGGCGA 836
Db 786 GCAGAAGGGGCGACGGGGAGGCCATCCCGCTGCACAGGTATGGGGTGGGTGAGCGGCGCT 845

QY 837 GCCCGCGCGCGCGG 852
Db 846 AGCGCTGAGCGCGG 861

RESULT 3

US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-09-165-543-3

Query Match 12.4%; Score 168; DB 3; Length 1335;
Best Local Similarity 51.4%; Pred. No. 3e-22;

Matches 440; Conservative 0; Mismatches 410; Indels 6; Gaps 2;

QY 3 GGCTCCCTGACGCGCGGCAACGAGCTGGAACGGGACCGAGCGCGCGCGG 62
Db 6 GCGCGCGCGCGCGCGCGCTGACCGCTTCGGGGCGCTGGCGGCGAGCGCGCG 65
QY 63 CGCGCGCGCGCGCGCGCGCTTACTTCCTGCGAGTGACGCTGAGCGTGTGCTGGCGG 122
Db 66 GCGCGCGCGCGCGCGCGCTTCGCGCAGCTGGAACCGCGGTGCTGGCGCGCTCATGCG 125
QY 123 CTGCTCATGCTGCTACCGTGTTCGGCAACGCTGCTGCTCATCATCGCGGTTCACGAG 182
Db 126 GCTGCTCATGCTGCGCGCGCGCTTCGCGCAGCTGGAACCGCGGTGCTGCTGCTGCGCGGA 185
QY 183 CGCGCGCGCTCAAGCGCGCGCGCGCGCGCTTCTCTGCTGCTGCTGCGCGCGCATCTCT 242
Db 186 CTGAGCGCTTCGCGCGCGCGCGCGCGCTTCTCTGCTCAACCTGCGCGCATCTCTGCTCTCT 245
QY 243 GGTGGCCACGCTCGTCTCATCCCTTTCTGCTGGCGCAACGAGGTGCTGCTGCTACTGTT 302

Db 246 CGTCGGCGCTTCTGCACTCCCACTGTATGTACCTACGTGCTGACAGCGCGCTGACCTT 305
QY 303 CGGCAAGGCTTGGTGGGAGATCTACCTGGCGCTCGAGTGTCTTCTGCGAGTGTGCTCAT 362
Db 306 CGGCGCGCGCGCTTCTGCAAGCTGTGGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 363 CGTGACCTGTGCGCCATCAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 366 CTTCAACATGCTGCTCATCAGCTAGGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
QY 423 C---AACCTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCATCATCATCATCATCATCAT 479
Db 426 CCGGCGCGCGCGCGCTGACACCG 485
QY 480 CTGCGCGCTCATCTCTCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
Db 486 GGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
QY 540 CCGCGAGCGCGCGCGCGCTGCGAGATCAACGACACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db 546 CATCCCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
QY 600 GTGATGCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Db 606 TTCCACCTGCGAGTCTTACGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
QY 660 CCAGATGCGCAAGCGTGGCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
Db 666 CTTGAACATCCAGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
QY 720 CG 776
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QY 777 GGGCG 836
Db 786 GCAGAAAGCG 845
QY 837 GCCCGCGCGCGCGCGG 852
Db 846 AGCGCTGAGCGCGCGG 861

RESULT 4

US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030


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QY 243 GTTGCCACGCTGTCATCCCTTTCTCGTGGCCAAACGAGGTCACTGCTACTGTTACTT 302
Db 536 CGTGGCGCTCTTGTGATCCCACTGATGTACCTACGTGCTGACAGCGCTGACACTT 595
QY 303 CGGCAAGGCTTGGTGGAGATCTACTGGCGGTGACAGTGTCTTCTGACGTCTCCAT 362
Db 596 CGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAGTACCTGTGTGACCTCTCTGCG 655
QY 363 CGTGACCTGTGGCCATCAGCTGACCGCTACTGCTCCATCACACAGGCCATCGAGTA 422
Db 656 CTTCACATCTGTCTCATCAGCTACGACCGCTTCTGTGGTCAACCGAGCGGTCTCATA 715
QY 423 C---AACCTGAAGCGCACCGCGCGCATCAAGGCCATCATCACCTGTGGGTGCT 479
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QY 480 CTGGCGGTCTCTCTTCCCGCGGTCTATCTCCATCGAGAAAGAGGGCGGGCGGG 539
Db 776 GGCCTTCTGTGTAGGACCAACCATCTGAGCTGGAGTACCTGTCCGGGGGAGCTC 835
QY 540 CCGCAGCGCGCGGAGCGCGCTGGAGATCAACGACAGAGTGGTACGTCTCTGTC 599
Db 836 CATCCCGAGGGCCACTGTATGCCAGTTCTTACAACTGGTACTTCTCTCATCACGGC 895
QY 600 GTGCATCGGCTCTTCTTCTCGTCCCTGCTCATCATGATCTCTGGTCTACGTGCGCATCTA 659
Db 896 TTCCACCTGGAGTTCTTTACGCCCTTCTCTACGCTGACCTTCTTTAACCCTCAGCATCTA 955
QY 660 CCAGATCGCAAGCTGCGACCGGGTGCACCCAGCGCGGGGTTCGGAGCGCGCTGCG 719
Db 956 CTTGAACATCCAGAGGCGCACCGCTCTCGGTGTAGTGGGCTCGAGAGGAGCGCGGCC 1015
QY 720 CGCGCGCGGGGGCACCGAGCGAGCGCCAAACGCTGTG---GGCCCCGAGCGCGCG 776
Db 1016 CGAGCCCCCTCCGAGGCCACCTCTACACCCCGCATCGCTGTGCTGTGGGTGCTG 1075
QY 777 GGGCCCCGGGGCGCAGAGCGCGCAACCGCTGCCACCCAGCTCAACGGCGCGCCCTGGCGA 836
Db 1076 GCAGAAAGGGGACGGGAGGCCATCCGCTGCACAGGTATGGGGTGGGTGAGGGCGCGT 1135
QY 837 GCCCGCGCGCGCGGG 852
Db 1136 AGCGCTGAGGCGCGG 1151
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RESULT 6

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; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
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US-09-167-354-6

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Query Match 12.3%; Score 166.4; DB 3; Length 1335;
Best Local Similarity 51.3%; Pred. No. 5.8e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;
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QY 3 GGGCTCCTCGACGCGACCGGGCAACGAGCTGAAACGGACGAGCGCGCGGGGG 62
Db 6 GCGCGCCCGCGACCGGCGCGTGAACGCTTCGGGGGCGCTGGCGGCGCATGCGGCGGC 65
QY 63 CGGCGCGCGGGCCACCCCTTACTCCCTGCAAGGTCAAGCTGACCTGTGTGCTTGGCGGG 122
Db 66 GGGGGGCGGGCGCGGGCTTCTCGGACGCTGGACCGGCTGCTGGCGCGCTCATGGC 125
QY 123 CTGTCTCATCTGCTCATCCGTGTTGGCAAGGTGCTGCTCATCATCGCCGTGTTACGAG 182
Db 126 GCTGCTCATCTGTTGGCCACGCTGTGGGCAACGGCGCTGCTCATGCTGCGCTTCTGCGCGA 185
QY 183 CCGCGCGCTCAAGGCGCGCCCAACCTCTTCTGCTGTCTCTGGCTCGGCGCTCGGCGCATCT 242
Db 186 CTGAGGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTTCCGACTTCT 245
QY 243 GGTGGCCACGCTCTGTCATCCCTTTCTCGTGGCCAAACGAGGTCACTGGGTACTTGGTACTT 302
Db 246 CGTGGCGCTTCTGCAATCCCACTGTATGTACCTACGTGCTGACAGCGCGCTGGACCTT 305
QY 303 CGGCAAGGCTTGGTGGAGATCTACCTGGGGCTCGAGGTGCTTCTTGAACGTGCTCCAT 362
Db 306 CGGCGGGGCGCTCTGCAAGCTGTGGCTGTGTGAGTACCTGCTGTGCACTCTCTGCTGC 365
QY 363 CGTGCACTGTGCGCCATCAGCTGACGCTGACCGCTACTGTGCTCATCACACAGGCCATCGAGTA 422
Db 366 CTTCACATCTGCTCATCAGCTACGACCGCTTCTGCTGCTCAGCGCGGTCTCATA 425
QY 423 C---AACCTGAAGCGCACCGCGCGCGCATCAAGGCCATCATCATCGTGTGGGTGCT 479
Db 426 CCGGGCCACGAGGGTGACACGCGCGGGGCGAGTGCAGAGATGCTGCTGTGTGGGTGCT 485
QY 480 CTGGCGGTCTATCTCTTCCCGCGCTCATCTCCATCGAGAAAGAGGGCGCGCGGGCGG 539
Db 486 GGCCTTCTCTGTATCGGACCAAGCATCTCTGAGCTGGGAGTACCTGCTCGGGGGGAGCTC 545
QY 540 CCGCAGCGCGCGCGAGCGCGCTGCGAGATCAACGACAGAGTGGTACGTATCTCTGCTC 599
Db 546 CATCCCGAGGGGCACTGTATGCCAGTTCTTCTAACAAGTGTACTTCTCATCACGGC 605
QY 600 GTGCATCGGCTCTTCTTCTGCTCCCTGCTCATCATGATCTCTGCTTACGTGCGCATCTA 659
Db 606 TTCCACCTCGAGTTCTTTAGGCCCTTCTCAGCGTCACTTCTTTAACCCTCAGCATCTA 665
QY 660 CCAGATCGCAAGCTGCGACCGCGCTGCCACCCAGCGCGGGGTCCGGAAGCGCGCTGC 719
Db 666 CTTGAACATCCAGAGGCGCACCGCGCTCCGGTGGATGGGGCTCGAGAGGAGCGCGCGCC 725
QY 720 CGCGCGCGGGGGCACCGAGCGAGGGCCCAACGCTGTG---GGCCCCGAGCGCGAGCGC 776
Db 726 CGAGCCCCCTCCCGAGGCCAGCCCTCACACCCCGCTGCTGTGGGTGCTGCTG 785
QY 777 GGGCCCCGGGGCGCAGAGCGCGAACCGTGTGCCACCCAGCTCAACGGCGCGCCCTGGCGA 836
Db 786 GCAGAAAGGGGACGGGAGGCCATGCCGTGACAGGTATGGGGTGGGTGAGGCGCGCT 845
QY 837 GCCCGCGCGCGCGGG 852
Db 846 AGCGCTGAGGCGCGG 861
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RESULT 7

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; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
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FILE REFERENCE: JMW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1335
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6

Query Match 12.3%; Score 166.4; DB 4; Length 1335;
Best Local Similarity 51.3%; Pred. No. 5.8e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCTGAGCGGACGCGGCAACGCGAGCTGGAAACGGACCGAGCGCGGGGG 62
DB 6 GCGGCGCGCGCGCGCGCTGACGCTTCGGGGCGCTGGCGGCGATGGCGGC 65
QY 63 CGGCGCGCGGCGCGCGCTTACTCCCTGCAAGTGACGCTGAGCGTGTGCTGCGCGGCGATCG 122
DB 66 GCGGCGCGGCGCGCGCTTCTCGGAGCGCTGACCGCGGCTGCGCGCGCTGCGCGGCG 125
QY 123 CTGCTCATGCTGCTACCGGTTGCGCAAGTGCTGCTCATCATCGCGTGTTCACGAG 182
DB 126 GCTGCTCATGCTGCGGCGCGCTGCGGCAACGCGCTGCTGCTGCTGCTGCTGCGCGCGA 185
QY 183 CCGCGCGCTCAAGCGCGCGCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
DB 186 CTCGAGCGCTCCGACCGCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 243 GGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
DB 246 GGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
QY 303 CGGCAAGGCTTGGTGGAGATTAAGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 362
DB 306 CGGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 365
QY 363 CGTGACCTGTGGCGCATCAGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 422
DB 366 CTTCAACATCGTGTCTCATCAGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 425
QY 423 C---AACCTGAAGCGCGCGCGCGCGCATCAAGCGCGCTGCGCGCGCTGCGCGCGCTGCG 479
DB 426 CCGGCG 485
QY 480 CTGCG 539
DB 486 GGCCTTCTGCTGACG 545

DB 786 CGAAGAGGGGACGCGGAGGCCATGCGCTGCACAGGTATGGGTGGGTGAGGCGCGCT 845
QY 837 GCGCGCGCGCGCGCGCGG 852
DB 846 AGGCGCTGAGCGCGG 861

RESULT 8
US-09-642-514-6
Sequence 6, Application US/09642514
Patent No. 6437100
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1335
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match 12.3%; Score 166.4; DB 4; Length 1335;
Best Local Similarity 51.3%; Pred. No. 5.8e-22;
Matches 439; Conservative 0; Mismatches 411; Indels 6; Gaps 2;

QY 3 GGGCTCCTGAGCGGACGCGGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 62
DB 6 GCGCGCGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 65
QY 63 CGGCGCGCGCGCGCGCGCTTACTCCCTGCAAGTGACGCTGAGCGTGTGCTGCGCGCG 122
DB 66 GCGGCGCGGCGCGCGGCTTCTCGGAGCGCTGACCGCGGCTGCGCGCGCTGCGCGCGCTGCG 125
QY 123 CTGCTCATGCTGCTACCGGTTGCGCAAGTGCTGCTCATCATCGCGTGTTCACGAG 182
DB 126 GCTGCTCATGCTGCGGCGCGCTGCGGCAACGCGCTGCTGCTGCTGCTGCTGCTGCGCGCGA 185
QY 183 CCGCGCGCTCAAGCGCGCGCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
DB 186 CTCGAGCGCTCCGACCGCGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 243 GGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
DB 246 GGTGGCGCGCTTCTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
QY 303 CGGCAAGGCTTGGTGGAGATTAAGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 362
DB 306 CGGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 365
QY 363 CGTGACCTGTGGCGCATCAGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 422
DB 366 CTTCAACATCGTGTCTCATCAGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
QY 423 C---AACCTGAAGCGCGCGCGCGCGCATCAAGCGCGCTGCGCGCGCTGCGCGCGCTGCG 479
DB 426 CCGGCG 485
QY 480 CTGCG 539
DB 486 GGCCTTCTGCTGACG 545

Db 1144 AGGCGCTGAGGCCGGG 1159

RESULT 12

US-08-475-742-15
; Sequence 15, Application US/08475742

; Patent No. 6121015

; GENERAL INFORMATION

APPLICANT: O'Malley

APPLICANT: Todd, Richard D

TITLE OF INVENTION: Gene Encod

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; FILE OR INVENTION: SOME ENCODING THE KAC DOPAMINE D4 RECEPTOR
; FILE REFERENCE: WU 102 CON DIV

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: CURRENT APPLICATION NUMBER: IIS

: CURRENT FILING DATE: 1995-06-07
 : CURRENT AFFILIATION NUMBER: US/08/413,142

EARLIER APPLICATION NUMBER: IIS

EARLIER FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: US 08/261,293

EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US

EARLIER FILING DATE: 1993-01-28
EARLIER APPLICATION NUMBER: US 08/014,013

: EARLIER FILING DATE: 1993-01-28
 : NUMBER OF SEQ ID NOS: 16

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: RAPOFT IN VOW

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; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 15

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; SEQ ID NO 15

; LENGTH: 2428

; TYPE: DNA

; ORGANISM: CDNA

; FEATURE:

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; NAME/KEY: misc_feature
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; LOCATION: (1) . . (2428)

OTHER INFORMATION: Rat d2 receptor sequence

; PUBLICATION INFORMATION:

TITLE: Cloning and expression of a rat D2 dopamine receptor

TITLE: CDNA.

JOURNAL: Nature

VOLUME: 336

PAGES: 783-787

DATE: 1988

DATE: 1988
US-08-475-742-15

Query Match 11.3%; Score 153; DB 3; Length 2428;
Best Local Similarity 48.8%; Pred. No. 1.6e-19;
Matches 594; Conservative 0; Mismatches 605; Indels 18; Gaps 6;

115	QY	CTGGCGGCGCTGCTCATGCTGTCTCACCGTGTTCGGCAACGTGCTCGTCAATCATGCCG	174
142	Db	CTGCTCACCGCTCTCATCTTTATCATCGCTTTGGCAATGTGCTGTGTCATGGCTGTA	201
175	QY	TTCAAGCGCGCGCTCAAGCGGCCCAAAACCTCTCTCGTGTGCTCTGCGCTCGGC	234
202	Db	TCCGAGAGAGGCTTTGCAGACACCACTACTTGTATGTACGCTTGCTGTGGCT	261
235	QY	GACATCCTGTGGCCACGCTCGTCACTCCCTTTCTGCTGCCAACAGGTCAATGGCTAC	294
262	Db	GATCTTTCTGTGGCCACACTGTGTAATGCGCTGGGTTGTCTACTCGAGGTGCTGGTGAG	321
295	QY	TGGTACTTTGGCAAGCGTTGGTCGAGATCTACCTGGCGCTCGAGTGTCTTCTTGCACG	354
322	Db	TGGAATTTAGCAGGATTCCTCTGTGACATCTTTGTCACTCTGGATGTATGATGTGCACA	381
355	QY	TCGTCCATCGTGCACTGTGCGGCATCAGCGCTGGACCGCTACTGTGTCCATCACAGGCC	414
382	Db	GCAAGCATCTGAACTGTGTGCCATCAGCATTTGACAGGTACACAGCTGTGGCAATGCC	441
415	QY	ATCGAGTACAAC---CTGAAGCGCAGCGCGCGCGCATCAAGGCCATCATCAACCGTG	471
442	Db	ATGCTGTATAACACACGCTACAGCTCCAAGCGCGAGTTACTGTATGATTTGCCATTTGTC	501
472	QY	TGGGTCACTCTGGCGCGTCACTCTCTCCCGCGCTCATCTCCATCGAGAAGAAGCGCGC	531
502	Db	TGGGTCTCTGCTTACCACATCTCTGCCACTGCTCTTCGGACTCAACATACAGACAG	561
532	QY	GGCGCGCGCGCAGCGCGCGAGCGCGCTCGAGATCAACGACAGAGTGGTACGTC	591
562	Db	AATGAGTG---TATCAATTGCCAACCTGCGCTTGTGGTCTACTCTCTCAATGCTCTCA	618


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QY 18 GGACGGGGCAACGAGCTGGAAACGGGACCGAGGGCCCGGGGGGGCGGGCCCGGGGCGAC 77
Db 387 GGAGCCGGGGAGCGGGGGCGGGCGGACGTGAATGGACGGGGCGCTCGGGGACT 446
QY 78 CCCTTACTCCCTGACGCTGAGCTGAGCTGGTGGCTGGCGGGCGCTGCTCATGCTGCT 137
Db 447 GGTGGTGGAGCGGCGGGCGTGGCGGTCTTCTGGGAGCG---TTTCATCTTAT 503
QY 138 CACCGGTGTTGGCAACGCTGCTCATCATCGCGTGTTCACGAGCGCGCGCTCAAGGC 197
Db 504 GGCGGTGGCAGGTAACTGCTTGTCTCATCTCTCAGTGGCTGCAACCGCCACTGCAGAC 563
QY 198 GCGCCAAAACCTTCTGCTGGTCTCTGGCTGCGCGGACATCTGCTGGGCGGCGCTGCT 257
Db 564 CGTCAACCACTATTTTCATCGTAACCTGGCGGCTGGCGGACCTGCTGCTGAGCGCACCGT 623
QY 258 CATCCCTTTCTCGCTGGCAACGAGCTGAGCTGAGTACTTCTGGCAAGGCTTGGT 317
Db 624 ACTGCCCTTCTCGGCGCACCATGGAGGTTCTGGGCTTCTGGGCGCTTGGCGCGCTTCTG 683
QY 318 CGAGATCTACTGCGCTCGACGCTGCTTCTGACGCTGCTTCTGACGCTGCTGACGCTGCGC 377
Db 684 CGAGTATGGCGCGCGCTGGAGCTGCTGCTGACGCGCTTCTGACGCGCTTCTGAC 743
QY 378 CATCAGCTGGACCGCTTACTGGTCCATCACAAGGCGCATCGAGTACAACTGAAGCGCAC 437
Db 744 CATCTCGTGGACCGGTACGTGGCGCTGGCGGCTGCGCCACTCACTCAAGTACCCAGCCATGAC 803
QY 438 GCGCGCGCGCATCAAGGCGCATCATCATCACCGTGTGGGTCTCTCGGCGCTCATCTCTT 497
Db 744 CATCTCGTGGACCGGTACGTGGCGCTGGCGGCTGCGCCACTCACTCAAGTACCCAGCCATGAC 803
QY 438 GCGCGCGCGCATCAAGGCGCATCATCATCACCGTGTGGGTCTCTCGGCGCTCATCTCTT 497
Db 804 CGAGCGCAAGCGCGCGCATCTCTGGGCTTCTGGGCTTCTGGGCGCTTGGCGCGCTTCTG 863
QY 498 CCGCGCGCTCATCTCCATCGAGAAGAGGCGGCGGCGGCGCGCGCGCGCGCGCGCGCG 557
Db 864 AGGGCGCTT-----GCTGGGCTGGAAGGAGCGCGCTGCGCGCTTCTGCGCG 908
QY 558 GCGCTGCGAGATCAACGACGAGGAGGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTTCTT 617

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RESULT 15

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US-08-468-939-1
; Sequence 1, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; NUMBER OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,939
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:
; US-08-468-939-1

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Query Match 11.2%; Score 151.8; DB 1; Length 2140;
Best Local Similarity 51.9%; Pred. No. 2.6e-19;
Matches 432; Conservative 0; Mismatches 377; Indels 24; Gaps 3;
QY 18 GGACGGGGCAACGAGCTGGAAACGGGACCGAGGGCCCGGGGGGGCGGGCCCGGGGCGAC 77
Db 387 GGAGCCGGGGAGCGGGCGGCGGCGGACGTGAATGGACGGGGCGCTCGGGGACT 446
QY 78 CCCTTACTCCCTGACGCTGAGCTGAGCTGGTGGCTGGCGGGCGCTGCTCATGCTGCT 137
Db 447 GGTGGTGGAGCGCGCGGCGTGGCGGTCTTCTGGGAGCG---TTTCATCTTAT 503
QY 138 CACCGGTGTTGGCAACGCTGCTCATCATCGCGTGTTCACGAGCGCGCGCTCAAGGC 197
Db 504 GGCGGTGGCAGGTAACTGCTTGTCTCATCTCTCAGTGGCTGCAACCGCCACTGCAGAC 563
QY 198 GCGCCAAAACCTTCTGCTGGTGTCTCTGGCTTCTGGCGCTGCGCGGACATCTTGGTGGCGCACGCTGCT 257
Db 564 CGTCAACCACTATTTTCATCGTAACCTGGCGGCTGGCGGACCTGCTGCTGAGCGCACCGT 623
QY 258 CATCCCTTTCTCGCTGGCAACGAGCTGAGCTGAGTACTTCTGGCAAGGCTTGGT 317
Db 624 ACTGCCCTTCTCGGCGCACCATGGAGGTTCTGGGCTTCTGGGCGCTTGGCGCGCTTCTG 683
QY 318 CGAGATCTACTGCGCTCGACGCTGCTTCTGACGCTGCTTCTGACGCTGCTGACGCTGCGC 377
Db 684 CGAGTATGGCGCGCGCTGGAGCTGCTGCTGACGCGCTTCTGACGCGCTTCTGAC 743
QY 378 CATCAGCTGGACCGCTTACTGGTCCATCACAAGGCGCATCGAGTACAACTGAAGCGCAC 437
Db 744 CATCTCGTGGACCGGTACGTGGCGCTGGCGGCTGCGCCACTCACTCAAGTACCCAGCCATGAC 803
QY 438 GCGCGCGCGCATCAAGGCGCATCATCATCACCGTGTGGGTCTCTCGGCGCTCATCTCTT 497
Db 804 CGAGCGCAAGCGCGCGCATCTCTGGGCTTCTGGGCTTCTGGGCGCTTGGCGCGCTTCTG 863
QY 498 CCGCGCGCTCATCTCCATCGAGAAGAGGCGGCGGCGGCGGCGCGCGCGCGCGCGCG 557
Db 864 AGGGCGCTT-----GCTGGGCTGGAAGGAGCGCGCTGCGCGCTTCTGCGCG 908
QY 558 GCGCTGCGAGATCAACGACGAGGAGGAGTGTGAGTGTGCTGCTGCTGCTGCTTCTT 617

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Thu Mar 13 13:27:54 2003

Db 909 CTTCTGCGGTATCACCGAGGAGCGGGCTACGCTGTCTTCTCCTCGTGTGCTCCTTCTA 968
Qy 618 CGCTCCCTGCTCATCATGATCTCTGTGCTACGTGCGCATCTACAGATCGC-----CAA 671
Db 969 CTTGCCCATGGCGGTATCTGTGCTCATGTACTGCCGCTGTAGTGTGCGGCGAGCAC 1028
Qy 672 GCCTGCGCACCCGCGTGCACCCAGCCGCGGGGTCCGGAGCGCCGTGCGCCGCGCCCGGG 731
Db 1029 CACCGCAGCTCGAGGCAGGCGTCAAGCGCGAGCGAGGCAAGGCCCTCCAGGTGTGCT 1088
Qy 732 GGGACCGAGCGAGGCGCCAAACGGTCTTGGGCCCCGAGCGAGCGCGGCGCCCGGGGGCGC 791
Db 1089 GCGCATCCACTGTCTCGGCGCGGCCACGGGCGCGGACGGGGCGCACGGCATGCGCAGCGC 1148
Qy 792 AGGGCCGAGCGGTGCGCCACCGCATCTACAGCGGCGCCCTGGCGAGCGCGCGC 844
Db 1149 CAAGGGCCACACTTCCGAGCTCGCTCTCCGTGCGCTGCTCAAGTTCTCCC 1201

Search completed: March 11, 2003, 07:41:17
Job time : 108.111 secs